

OM protein - protein search, using sw model  
Run on: August 28, 2006, 17:25:54 ; Search time 196 Seconds  
(without alignments)  
620.508 Million cell updates/sec

Title: US-10-006-867-2  
Perfect score: 1392  
Sequence: 1 MMWFQQLSFLPSALVIWTS.....YDTAPCPINNERTLLSRDI 266  
Scoring table: BLOSUM62  
Searched: Gapop 10.0 , Gapext 0.5  
Total number of hits satisfying chosen parameters: 2589679  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_8.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAY66636	standard; protein; 266 AA.				
DE	Membrane-bound protein PRO180.					
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 3;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT 2						
ID	AAU29028	standard; protein; 266 AA.				
DE	Human PRO polypeptide sequence #5.					
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 3;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT 3						
ID	AAM39568	standard; protein; 266 AA.				
DE	Human polypeptide SEQ ID NO 2713.					
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1392;	DB 4;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT 4						
ID	AAB65159	standard; protein; 266 AA.				
DE	Human PRO180 (UNQ154) protein sequence SEQ ID NO:23.					
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 4;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT 5						
ID	ABB90338	standard; protein; 266 AA.				
DE	Human polypeptide SEQ ID NO 2714.					
PN	WO200190304-A2.					
PD	29-NOV-2001.					
PA	(HUMA-) HUMAN GENOME SCI INC.					
Query Match	100.0%;	Score 1392;	DB 5;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 5e-149;				
RESULT 6						
ID	ABG95851	standard; protein; 266 AA.				
DE	Human secreted/transmembrane protein PRO180.					

PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 5; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 7  
ID ABU58404 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 8  
ID ABU87952 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 9  
ID ABU84267 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 10  
ID ABR66141 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 11  
ID ABR65531 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 12  
ID ABU99471 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 13  
ID ABU57974 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 14  
ID ABU59052 standard; protein; 266 AA.  
DE Novel human secreted or transmembrane protein PRO180.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 15  
ID ABU82564 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 16  
ID ABU82710 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032113-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 17  
ID ABU9831 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 18  
ID ABR68080 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 19  
ID ADA57044 standard; protein; 266 AA.  
DE Human secreted protein #327.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 20  
ID ABU60483 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 21  
ID ABU96133 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 22  
ID ABU92564 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 23  
ID ABO08641 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 24  
ID ABO02693 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 25  
ID ABR74847 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 26  
ID ABR94609 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044926-A1.  
PD 06-MAR-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 27  
ID ABU13865 standard; protein; 266 AA.  
DE Human PRO180 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 28  
ID ABU85582 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 29  
ID ABU98742 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 30  
ID ABU97957 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 31  
ID ABU91663 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 32  
ID ABU89356 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 33  
ID ABU86197 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 34  
ID ABU67410 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 35  
ID ABU80438 standard; protein; 266 AA.  
DE Human PRO protein #5.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 36  
ID ABU72450 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.



PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 37  
ID ABU90876 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 38  
ID ABO33935 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 39  
ID ABR99356 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 40  
ID ABR98746 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 41  
ID ABO16269 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 42  
ID ABR92169 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 43  
ID ABO18810 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 44  
ID ABR78231 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 45  
ID ABU71952 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 46

ID ABU84967 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 47  
ID ABO00106 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 48  
ID ABO11438 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 49  
ID ABO02083 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 50  
ID ADA40898 standard; protein; 266 AA.  
DE Human secreted protein.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 51  
ID ABU88657 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 52  
ID ABU83352 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 53  
ID ABO06153 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 54  
ID ABR59189 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 55  
ID ABO09251 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 56  
ID ABO19115 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.

PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 57  
ID ABO11133 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 58  
ID ABR66751 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 59  
ID ABO15964 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 60  
ID ABO13670 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 61  
ID ABU71506 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 62  
ID ABU65573 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein, SEQ ID 10.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 63  
ID ABO07421 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 64  
ID ABO03608 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 65  
ID ABR67056 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 66  
ID ABO13980 standard; protein; 266 AA.  
DE Novel human secreted protein #9.  
PN US2003028003-A1.

PD 06-FEB-2003.  
PA (ROSE/) ROSEN C A.  
PA (FENG/) FENG P.  
PA (RUBE/) RUBEN S M.  
PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H S.  
PA (NIJJ/) NI J.  
PA (WEIY/) WEI Y.  
PA (SOPP/) SOPPET D R.  
PA (MOOR/) MOORE P A.  
PA (KYAW/) KYAW H.  
PA (LAFL/) LAFLEUR D W.  
PA (SHIY/) SHI Y.  
PA (JANA/) JANAT F.  
PA (ENDR/) ENDRESS G A.  
PA (CART/) CARTER K C.  
PA (BIRS/) BIRSE C E.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 67  
ID ABO15659 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 68  
ID ABU55940 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein, PRO180.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 69  
ID ABU72287 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 70  
ID ABU65268 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 71  
ID ABU95213 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 72  
ID ABU71116 standard; protein; 266 AA.  
DE Human PRO180 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 73  
ID ABO07726 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 74  
ID ABR69967 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 75  
ID ABR69300 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 76  
ID ABO01441 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 77  
ID ABU81243 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 78  
ID ABR60040 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 79  
ID ABU90960 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 80  
ID ABR67775 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 81  
ID ABR65163 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 82  
ID ABR68385 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 83  
ID ABR71797 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 84  
ID ABU59199 standard; protein; 266 AA.

DE Human secreted/transmembrane protein, #9.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 85  
ID ABU85277 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 86  
ID ABU88967 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 87  
ID ABU83047 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 88  
ID ABU94903 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 89  
ID ABU90451 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 90  
ID ABU83962 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 91  
ID ABU93613 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 92  
ID ABO25896 standard; protein; 266 AA.  
DE Human PRO180 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 93  
ID ABR64858 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 94  
ID ABO27281 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO180.

PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 95  
ID ABR68690 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 96  
ID ABO06506 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 97  
ID ABR99051 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 98  
ID ABU56935 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 99  
ID ABU85887 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 100  
ID ABU82174 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 101  
ID ABU87185 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 102  
ID ABU83657 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 103  
ID ABO08031 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 104  
ID ABU92476 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003045684-A1.  
PD 06-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 105  
ID ABU81742 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 106  
ID ABU65906 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 107  
ID ABU81146 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 108  
ID ABR59735 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 109  
ID ABU93923 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 110  
ID ABU99776 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 111  
ID ABR66446 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 112  
ID ABR90864 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 113  
ID ABO53261 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 114  
ID ABU58905 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein, #9.  
PN US2002142961-A1.

PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 115  
ID ABU94291 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 116  
ID ABU79173 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 117  
ID ABU86502 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 118  
ID ABU86807 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 119  
ID ABU94596 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 120  
ID ABO04523 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 121  
ID ABR70272 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 122  
ID ABU92283 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 123  
ID ABU98437 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 124  
ID ABR65836 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 125  
ID ABR64553 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 126  
ID ABU59348 standard; protein; 266 AA.  
DE Novel human secreted or transmembrane protein PRO180.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 127  
ID ABU79478 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 128  
ID ABU92869 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 129  
ID ABU95828 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 130  
ID ABU91048 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 131  
ID ABU90141 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 132  
ID ABO09556 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 133  
ID ABO10828 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 134  
ID ABR70882 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 135



ID ABU98263 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 136  
ID ABU87490 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 137  
ID ABU91358 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 138  
ID ABU99268 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 139  
ID ABU84572 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 140  
ID ABR69662 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 141  
ID ABU80039 standard; protein; 266 AA.  
DE Human PRO protein #5.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 142  
ID ABU82475 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 143  
ID ABU92114 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 144  
ID ABU93308 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 145

ID ABO09861 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 146  
ID ABO08946 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 147  
ID ABU96439 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 148  
ID ABU10820 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 149  
ID ABU10514 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein #5.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 150  
ID ABU81572 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 151  
ID ABU72109 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 152  
ID ABU95523 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 153  
ID ABU96732 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 154  
ID ABR70577 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 155
ID ABO04928 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 156
ID ABO08336 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 157
ID ABU88511 standard; protein; 266 AA.
DE Human secreted and transmembrane polypeptide PRO180.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 158
ID ABO34025 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 159
ID ABO05543 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 160
ID ABR73932 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 161
ID ABR95524 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 162
ID ABR80821 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 163
ID ABR81126 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 164
ID ABM00822 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073180-A1.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 165
ID ABR88424 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 166
ID ABM77245 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 167
ID ABO28729 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 168
ID ABO31474 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 169
ID ABM07891 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 170
ID ABO40371 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 171
ID ABO35796 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 172
ID ABO43935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 173
ID ADA7762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073180-A1.
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PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 174  
ID ABM24730 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 175  
ID ABO02998 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 176  
ID ABR90254 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 177  
ID ABM17168 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 178  
ID ABR94914 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 179  
ID ABR95219 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 180  
ID ADBI7059 standard; protein; 266 AA.  
DE Human transmembrane PRO polypeptide (SeqID 2).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 181  
ID ABO21457 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 182  
ID ABR97721 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 183

ID ABR87509 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 184  
ID ABM77550 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 185  
ID ABM27780 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 186  
ID ABM06061 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 187  
ID ABM03567 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 188  
ID ABM35018 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 189  
ID ABM26255 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 190  
ID ABO48037 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 191  
ID ABR92779 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 192  
ID ABO24540 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 193  
ID ADA37534 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 194  
ID ABM11551 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 195  
ID ABM02652 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 196  
ID ABM15948 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 197  
ID ABO27509 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 198  
ID ABM29000 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 199  
ID ABM06976 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 200  
ID ABM21070 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 201  
ID ABM09416 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073175-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 202  
ID ABO41286 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 203  
ID ABO36101 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 204  
ID ABO43630 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 205  
ID ABM76330 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 206  
ID ABM76026 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 207  
ID ABM25645 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 208  
ID ABM25950 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 209  
ID ADA21220 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO180.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 210  
ID ABO03303 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 211  
ID ABO02388 standard; protein; 266 AA.

DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040061-A1.  
PD 27-FEB-2003. Length 266;  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 212  
ID ABO44239 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO 180.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 213  
ID ABR90559 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 214  
ID ABR73627 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 215  
ID ABO16879 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 216  
ID ABR94304 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 217  
ID ABR75811 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 218  
ID ABR71187 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 219  
ID ABR93084 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 220  
ID ABR93389 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 221  
ID ADA10007 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein, PRO180.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 222  
ID ABR87814 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 223  
ID ABO27814 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 224  
ID ABO29949 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 225  
ID ABO33158 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 226  
ID ABM04846 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 227  
ID ABM08806 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 228  
ID ABO36406 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 229  
ID ABO35491 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;  
RESULT 230  
ID ABO35491 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
LENGTH 266;



ID ABO39456 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 231  
ID ABM10331 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 232  
ID ABM11856 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 233  
ID ABO52002 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 234  
ID ABO52307 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 235  
ID ADA19864 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 236  
ID ABO23625 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 237  
ID ADB17247 standard; protein; 266 AA.  
DE Human transmembrane PRO polypeptide (SeqID 2).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 238  
ID ADA17551 standard; protein; 266 AA.  
DE Human PRO180 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 239  
ID ABR97111 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054481-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 240  
ID ABR86899 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 241  
ID ABM10941 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 242  
ID ABM28085 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 243  
ID ABO32084 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 244  
ID ABM15211 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 245  
ID ABM06366 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 246  
ID ABM04177 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 247  
ID ABM22290 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 248  
ID ABM07586 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068751-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 249  
ID ABO40676 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 250  
ID ABM35323 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 251  
ID ABM33086 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 252  
ID ABO52612 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 253  
ID ABO50172 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 254  
ID ABU99166 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 255  
ID ABO4218 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 256  
ID ABO05848 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 257  
ID ABM18388 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 258  
ID ADA27659 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 259  
ID ABR97416 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 260  
ID ABR80516 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 261  
ID ABM01127 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 262  
ID ABR88729 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 263  
ID ABM13381 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 264  
ID ABM20765 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 265  
ID ABO41896 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 266  
ID ABO42506 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 267  
ID ABM10026 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003067478-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 268
ID ABO38541 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 269
ID ABM32781 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 270
ID ABM22595 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087373-A1.
PD 08-MAY-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 271
ID ABM74806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096353-A1.
PD 22-MAY-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 272
ID ADA79554 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073173-A1.
PD 17-APR-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 273
ID ABR96196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054458-A1.
PD 20-MAR-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 274
ID ABM02347 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 275
ID ABR86289 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 276
ID ABR86594 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 277
ID ABM16558 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 278
ID ABM29610 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 279
ID ABO29034 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 280
ID ABM23815 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 281
ID ABM23205 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 282
ID ABM21985 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 283
ID ABO37626 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 284
ID ABM28390 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082715-A1.
PD 01-MAY-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 285
ID ABM28695 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082716-A1.
PD 01-MAY-2003.
  Query Match      100.0%; Score 1392; DB 6; Length 266;
  Best Local Similarity 100.0%; Pred. No. 5e-149;
RESULT 286
ID ABM66339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068737-A1.
PD 10-APR-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 287  
ID ABM75721 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 288  
ID ABM34001 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 289  
ID ABM34306 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 290  
ID ABO20237 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 291  
ID ABO21152 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 292  
ID ABO22067 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 293  
ID ADA20036 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 294  
ID ABO34167 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO 180.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 295  
ID ABR96501 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 296  
ID ADA94239 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 297  
ID ABR85679 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 298  
ID ABR99661 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 299  
ID ABM00212 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 300  
ID ABM00517 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 301  
ID ABO29644 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 302  
ID ABM23510 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 303  
ID ABM29305 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 304  
ID ABO38236 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 305  
ID ABO45536 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003073182-A1.

PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 306  
ID ABM20460 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 307  
ID ADA81281 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 308  
ID ABO16574 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 309  
ID ABO18200 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 310  
ID ABO22627 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 311  
ID ABO22932 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 312  
ID ABR92474 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 313  
ID ABR81431 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 314  
ID ABM77855 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 315  
ID ABR89644 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 316  
ID ABM26560 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 317  
ID ABM13686 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 318  
ID ABO28424 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 319  
ID ABO30254 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 320  
ID ABM07281 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 321  
ID ABM03872 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 322  
ID ABO37016 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 323  
ID ABO41591 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 324  
ID ABO35186 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.







Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 363  
ID ABO25590 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 364  
ID ABR93999 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 365  
ID ADA92585 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 366  
ID ABR79906 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 367  
ID ABM11246 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 368  
ID ABO32853 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 369  
ID ABO30559 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 370  
ID ABO30864 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 371  
ID ABM27170 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 372  
ID ABM29915 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 373  
ID ABM05451 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 374  
ID ABM15516 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 375  
ID ABM08501 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 376  
ID ABO42201 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 377  
ID ABO37931 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 378  
ID ABO45841 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 379  
ID ABM66644 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 380  
ID ADB20122 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 381  
ID ABM19545 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104552-A1.

PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 382  
ID ABO49257 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 383  
ID ABO49562 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 384  
ID ADA78374 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 385  
ID ABR88119 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 386  
ID ADA00333 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO 180.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 387  
ID ABM26865 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 388  
ID ABM03262 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 6; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 389  
ID ABO39761 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 390  
ID ABO49867 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049776-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 391  
ID ABO50782 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 392  
ID ABO05238 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 393  
ID ABR74542 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 394  
ID ABR77021 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 395  
ID ABM17778 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 396  
ID ABR95829 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 397  
ID ABO21762 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 398  
ID ABO19932 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 399  
ID ABO24235 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 400  
ID ABR85984 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049759-A1.





PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 420  
ID ABR87204 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 421  
ID ABM12771 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 422  
ID ABM30525 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 423  
ID ABM24425 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 424  
ID ABO29339 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 425  
ID ABO31169 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 426  
ID ABM14296 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 427  
ID ABM09721 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 428  
ID ABO38846 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068774-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 429  
ID ABM34611 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 430  
ID ABO51087 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 431  
ID ABO03913 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 432  
ID ABO10383 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 433  
ID ABO53111 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 434  
ID ABR77626 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 435  
ID ABR78836 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 436  
ID ABO23930 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 437  
ID ABR93694 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 438  
ID ABM01737 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 439  
ID ABM78160 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 440  
ID ABR89949 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 441  
ID ADA22146 standard; protein; 266 AA.  
DE Human secreted/transmembrane polypeptide PRO180.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 442  
ID ABM27475 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 443  
ID ABM13076 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 444  
ID ABO31779 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 445  
ID ABM13991 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 446  
ID ABM08196 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 447  
ID ABO40066 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 448  
ID ABM74501 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 449  
ID ABM33696 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 450  
ID ABM20155 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 451  
ID ABO48647 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 452  
ID ABO22481 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 453  
ID ABR72712 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 454  
ID ABO15354 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 455  
ID ABR85069 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 456  
ID ABO15049 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 457  
ID ABO17184 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003040077-A1.

PD 27-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 458  
ID ABM17473 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 459  
ID ADA06312 standard; protein; 266 AA.  
DE Human secreted/transmembrane PRO polypeptide #6.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 460  
ID ADA39005 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 461  
ID ABR85374 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 462  
ID ABM76940 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 463  
ID ABO28119 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 464  
ID ABM22900 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 465  
ID ABM30220 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 466  
ID ABM21680 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 467

ID ABM21375 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 468  
ID ABM14906 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 469  
ID ABO40981 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 470  
ID ABO36711 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 471  
ID ABO37321 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 472  
ID ABM75111 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 473  
ID ABM33391 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 474  
ID ABO46146 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 475  
ID ADA82445 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 476  
ID ADB85575 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 477  
ID ADB96031 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 478  
ID ABM31745 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 479  
ID ABM31135 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 480  
ID ADB85753 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 481  
ID ABM32050 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 482  
ID ABM32355 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 483  
ID ADB68254 standard; protein; 266 AA.  
DE Human PRO180 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 484  
ID ADB68061 standard; protein; 266 AA.  
DE Human PRO180 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 485  
ID ABM31440 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068761-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 486  
ID ABM30830 standard; protein; 266 AA.  
DE Human secreted polypeptide PRO180, SEQ ID NO:10.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 487  
ID ADB90878 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 488  
ID ADC57503 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 489  
ID ADC54867 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 490  
ID ADC11734 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 491  
ID ADC06958 standard; protein; 266 AA.  
DE Human PRO180 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 492  
ID ADC56156 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 493  
ID ADC17137 standard; protein; 266 AA.  
DE Mammalian PRO polypeptide (SeqID 2).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 494  
ID ADC07211 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 495  
ID ADC11201 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.

PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 496  
ID ADC14835 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 497  
ID ADC52330 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 498  
ID ADC14323 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 499  
ID ADD07855 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 500  
ID ADC81680 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 501  
ID ADD07322 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 502  
ID ADC82213 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 503  
ID ADD05483 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 504  
ID ADC78249 standard; protein; 266 AA.  
DE Human secreted protein SEQ ID NO:56.  
PN WO2003072761-A1.  
PD 04-SEP-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 505

ID ADD08393 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 506  
ID ADD06642 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 507  
ID ADC82889 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 508  
ID ADD54996 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 509  
ID ADD36006 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 510  
ID ADD55954 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 511  
ID ADD54392 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 512  
ID ADE26546 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 513  
ID ADE26013 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 514  
ID ADF66950 standard; protein; 266 AA.  
DE Human PRO180 amino acid sequence SEQ ID NO:23.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;



RESULT 515  
ID ADG01007 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 516  
ID ADG08560 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 517  
ID ADG02478 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 518  
ID ADG01185 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 519  
ID ADF95360 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 520  
ID ADF95181 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 521  
ID ADG12175 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 522  
ID ADH24034 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 523  
ID ADH34060 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 524  
ID ADH29893 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 525  
ID ADH23864 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 526  
ID ADH08835 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 527  
ID ADG85268 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 528  
ID ADH24544 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 529  
ID ADH37400 standard; protein; 266 AA.  
DE Human secreted and transmembrane protein PRO180.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 530  
ID ADH01989 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 531  
ID ADH37570 standard; protein; 266 AA.  
DE Human secreted and transmembrane protein PRO180.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 532  
ID ADG85608 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 533  
ID ADH24204 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.

PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 534  
ID ADH38498 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 535  
ID ADG83619 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 536  
ID ADH29427 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 537  
ID ADH27543 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 538  
ID ADH37740 standard; protein; 266 AA.  
DE Human secreted and transmembrane protein PRO180.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 539  
ID ADH37917 standard; protein; 266 AA.  
DE Human secreted and transmembrane protein PRO180.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 540  
ID ADH57337 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 541  
ID ADH53479 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 542  
ID ADH53649 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181641-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 543  
ID ADH51985 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 544  
ID ADH49840 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 545  
ID ADI25350 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 546  
ID ADH90143 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 547  
ID ADI25520 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 548  
ID ADH97694 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 549  
ID ADI35204 standard; protein; 266 AA.  
DE Human PRO polypeptide #6.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 550  
ID ADI03542 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 551  
ID ADI11899 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 552  
ID ADH98973 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 553  
ID ADH99696 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 554  
ID ADH98374 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 555  
ID ADI11049 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 556  
ID ADI11559 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 557  
ID ADH98204 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 558  
ID ADH98544 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 559  
ID ADH98034 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 560  
ID ADI05022 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 561  
ID ADI03372 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 562  
ID ADI04767 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 563  
ID ADH78221 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181668-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 564  
ID ADI19565 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 565  
ID ADH90313 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 566  
ID ADI03032 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 567  
ID ADH77881 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 568  
ID ADH97864 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 569  
ID ADI01249 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 570  
ID ADI03372 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;

ID ADI01944 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 571  
ID ADI03202 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 572  
ID ADI11389 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 573  
ID ADI02291 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 574  
ID ADI11729 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 575  
ID ADI05366 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 576  
ID ADH79438 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 577  
ID ADI19395 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 578  
ID ADI05196 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 579  
ID ADH79608 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 580  
ID ADI01434 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 581  
ID ADI01604 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 582  
ID ADI01774 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 583  
ID ADH79778 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 584  
ID ADI04596 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 585  
ID ADI02732 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 586  
ID ADH78051 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 587  
ID ADI25690 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 588  
ID ADI25860 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.

PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 589  
ID ADK65372 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 590  
ID ADH98714 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 591  
ID ADH79955 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 592  
ID ADL32616 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 593  
ID ADM30150 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 594  
ID ADL93686 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 7; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 595  
ID ADC52140 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 596  
ID ADE74147 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 597  
ID ADE74759 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein (PRO) #5.  
PN US2003211574-A1.  
PD 13-NOV-2003.

Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 598  
ID ADF35149 standard; protein; 266 AA.  
DE Human PRO180 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 599  
ID ADG11399 standard; protein; 266 AA.  
DE Human PRO180 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 600  
ID ADF95972 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 601  
ID ADG04243 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 602  
ID ADG00403 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 603  
ID ADH06572 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 604  
ID ADH06402 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 605  
ID ADG68823 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 606  
ID ADH27713 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 607  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;



ID ADH25054 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 608  
ID ADH33686 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 609  
ID ADG82659 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 610  
ID ADH02329 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 611  
ID ADH07936 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 612  
ID ADG69333 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 613  
ID ADH39154 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 614  
ID ADH25940 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 615  
ID ADG83894 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 616  
ID ADH19269 standard; protein; 266 AA.

DE Human secreted/transmembrane protein PRO180.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 617  
ID ADG85438 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 618  
ID ADH06232 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 619  
ID ADH30063 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 620  
ID ADH24374 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 621  
ID ADH32909 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 622  
ID ADG69503 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 623  
ID ADH07766 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 624  
ID ADG85778 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 625  
ID ADH39324 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.

PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 626  
ID ADH33516 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 627  
ID ADH33856 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 628  
ID ADH01066 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 629  
ID ADG69673 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 630  
ID ADH20762 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 631  
ID ADH02159 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 632  
ID ADG69163 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 633  
ID ADG85948 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 634  
ID ADH24884 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180909-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 635  
ID ADH39501 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 636  
ID ADH19802 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein PRO180.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 637  
ID ADH02499 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 638  
ID ADG68993 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 639  
ID ADH07596 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 640  
ID ADG86118 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 641  
ID ADH24714 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 642  
ID ADH25762 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 643  
ID ADH38328 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 644  
ID ADH38328 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 644  
ID ADH57167 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 645  
ID ADH52155 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 646  
ID ADH49521 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 647  
ID ADH90483 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 648  
ID ADI11219 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 649  
ID ADH98884 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 650  
ID ADI02114 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 651  
ID ADH90653 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 652  
ID ADJ54648 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;

Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 653  
ID ADJ98528 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 654  
ID ADJ98698 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 655  
ID ADH78857 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 656  
ID ADJ99091 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 657  
ID ADJ99261 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 658  
ID ADJ98879 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 659  
ID ADH79027 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 660  
ID ADK00887 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 661  
ID ADK14408 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;

RESULT 662  
ID ADJ64419 standard; protein; 266 AA.  
DE Human PRO polypeptide #5.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 663  
ID ADM31315 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 664  
ID ADM36362 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 665  
ID ADM40167 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 666  
ID ADM80857 standard; protein; 266 AA.  
DE Human PRO polypeptide #1.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 667  
ID ADN60677 standard; protein; 266 AA.  
DE Human secreted polypeptide #9.  
PN US2004038277-A1.  
PD 26-FEB-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 668  
ID ADN37775 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 8; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 669  
ID ADY77697 standard; protein; 266 AA.  
DE Neoplastic disease detection protein PRO180.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1392; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 670  
ID ADY77697 standard; protein; 266 AA.  
DE Neoplastic disease detection protein PRO180.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1392; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 670

ID AEA38350 standard; protein; 266 AA.  
DE Human secreted/transmembrane protein CDNA, #73.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 671  
ID AED11495 standard; protein; 266 AA.  
DE Human gene 26 encoded secreted protein HCPCI91, SEQ ID NO: 56.  
PN US2005214786-A1.  
PD 29-SEP-2005.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 672  
ID AED50005 standard; protein; 266 AA.  
DE Novel human secreted and transmembrane protein PRO180.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 9; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 673  
ID AEF12528 standard; protein; 266 AA.  
DE Human PRO180 protein SEQ ID NO:2.  
PN US2006008901-A1.  
PD 12-JAN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1392; DB 10; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 674  
ID AEF74217 standard; protein; 266 AA.  
DE Human PRO180 protein SEQ ID NO:2.  
PN US2005260647-A1.  
PD 24-NOV-2005.  
PA (EATO/) EATON D L.  
PA (FILV/) FILVAROFF E.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W L.  
Query Match 100.0%; Score 1392; DB 10; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 675  
ID AAY27575 standard; protein; 267 AA.  
DE Human secreted protein encoded by gene No. 9.  
PN WO9924836-A1.  
PD 20-MAY-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 100.0%; Score 1392; DB 2; Length 267;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 676  
ID ADG78386 standard; protein; 267 AA.  
DE Human secreted protein #9.  
PN US2003211472-A1.  
PD 13-NOV-2003.  
PA (FENG/) FENG P.  
PA (RUBE/) RUBEN S M.  
PA (ROSE/) ROSEN C A.  
PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H S.  
PA (NIJJ/) NI J.  
PA (WEIY/) WEI Y.  
PA (SOPP/) SOPPET D R.  
PA (MOOR/) MOORE P A.  
PA (KYAW/) KYAW H.  
PA (LAFL/) LAFLEUR D W.  
PA (SHIY/) SHI Y.  
PA (JANA/) JANAT F.  
PA (ENDR/) ENDRRESS G A.

PA (CART/) CARTER K C. 100.0%; Score 1392; DB 8; Length 267;  
Query Match 100.0%; Pred. No. 5e-149;  
Best Local Similarity 100.0%; Pred. No. 5e-149;  
RESULT 677  
ID ABB12041 standard; peptide; 275 AA.  
DE Human secreted protein homologue, SEQ ID NO:2411.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. 100.0%; Score 1392; DB 4; Length 275;  
Query Match 100.0%; Pred. No. 5.2e-149;  
Best Local Similarity 100.0%; Pred. No. 5.2e-149;  
RESULT 678  
ID AAM41354 standard; protein; 275 AA.  
DE Human polypeptide SEQ ID NO 6285.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC. 100.0%; Score 1392; DB 4; Length 275;  
Query Match 100.0%; Score 1392; DB 4; Length 275;  
Best Local Similarity 100.0%; Pred. No. 5.2e-149;  
RESULT 679  
ID AAB87526 standard; protein; 266 AA.  
DE Human PRO180.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC. 99.9%; Score 1390; DB 4; Length 266;  
Query Match 99.9%; Score 1390; DB 4; Length 266;  
Best Local Similarity 99.6%; Pred. No. 8.4e-149;  
RESULT 680  
ID AAY36185 standard; protein; 267 AA.  
DE Human secreted protein #57.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET. 99.7%; Score 1388; DB 2; Length 267;  
Query Match 99.7%; Score 1388; DB 2; Length 267;  
Best Local Similarity 99.6%; Pred. No. 1.4e-148;  
RESULT 681  
ID ADJ46037 standard; protein; 267 AA.  
DE Novel human secreted protein-related protein sequence SeqID190.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M. 99.7%; Score 1388; DB 2; Length 267;  
PA (DUCL/) DUCLERT A. 99.6%; Pred. No. 1.4e-148;  
PA (BOUG/) BOUGUELERET L. 99.7%; Score 1388; DB 7; Length 267;  
Query Match 99.7%; Score 1388; DB 7; Length 267;  
Best Local Similarity 99.6%; Pred. No. 1.4e-148;  
RESULT 682  
ID ADP19446 standard; protein; 267 AA.  
DE Human secreted polypeptide #297.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST ) GENSET SA. 99.7%; Score 1388; DB 8; Length 267;  
Query Match 99.7%; Score 1388; DB 8; Length 267;  
Best Local Similarity 99.6%; Pred. No. 1.4e-148;  
RESULT 683  
ID AAY29866 standard; protein; 208 AA.  
DE Human secreted protein clone pe318\_4.  
PN WO9946287-A1.  
PD 16-SEP-1999.  
PA (GEMY ) GENETICS INST INC. 77.4%; Score 1078; DB 2; Length 208;  
Query Match 77.4%; Score 1078; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 1.6e-113;  
RESULT 684  
ID ABP75476 standard; protein; 166 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 660.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC. 58.6%; Score 816; DB 6; Length 166;  
Query Match 58.6%; Score 816; DB 6; Length 166;  
Best Local Similarity 93.4%; Pred. No. 6.8e-84;  
RESULT 685  
ID AAB88330 standard; protein; 136 AA.  
DE Human membrane or secretory protein clone PSEC0031.  
PN EP1067182-A2.

PD 10-JAN-2001.  
PA (HELI-) HELIX RES INST. 52.1%; Score 725; DB 4; Length 136;  
Query Match 52.1%; Score 725; DB 4; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.1e-73;  
RESULT 686  
ID ADY63025 standard; protein; 136 AA.  
DE Human clone PSEC0031 protein, SEQ ID 28.  
PN EP1514933-A1.  
PD 16-MAR-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 52.1%; Score 725; DB 9; Length 136;  
Query Match 52.1%; Score 725; DB 9; Length 136;  
Best Local Similarity 100.0%; Pred. No. 1.1e-73;  
RESULT 687  
ID AAY36138 standard; protein; 172 AA.  
DE Human secreted protein #10.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET. 42.8%; Score 595.5; DB 2; Length 172;  
Query Match 42.8%; Score 595.5; DB 2; Length 172;  
Best Local Similarity 79.4%; Pred. No. 8e-59;  
RESULT 688  
ID ADJ45943 standard; protein; 172 AA.  
DE Novel human secreted protein-related protein sequence SeqID96.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M. 42.8%; Score 595.5; DB 7; Length 172;  
PA (DUCL/) DUCLERT A. 79.4%; Pred. No. 8e-59;  
PA (BOUG/) BOUGUELERET L. 42.8%; Score 595.5; DB 7; Length 172;  
Query Match 42.8%; Score 595.5; DB 7; Length 172;  
Best Local Similarity 79.4%; Pred. No. 8e-59;  
RESULT 689  
ID ADM04182 standard; protein; 238 AA.  
DE Human protein of the invention SEQ ID NO:2867.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 34.9%; Score 486.5; DB 7; Length 238;  
Query Match 34.9%; Score 486.5; DB 7; Length 238;  
Best Local Similarity 38.6%; Pred. No. 3e-46;  
RESULT 690  
ID AEC87112 standard; protein; 238 AA.  
DE Human cDNA clone protein BRIOC20101230, SEQ ID 2867.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 34.9%; Score 486.5; DB 9; Length 238;  
Query Match 34.9%; Score 486.5; DB 9; Length 238;  
Best Local Similarity 38.6%; Pred. No. 3e-46;  
RESULT 691  
ID AAE26425 standard; protein; 231 AA.  
DE Human transmembrane protein (TMP)-11 protein.  
PN WO200234783-A2.  
PD 02-MAY-2002.  
PA (INCY-) INCYTE GENOMICS INC. 34.5%; Score 480.5; DB 5; Length 231;  
Query Match 34.5%; Score 480.5; DB 5; Length 231;  
Best Local Similarity 38.7%; Pred. No. 1.4e-45;  
RESULT 692  
ID ADK70499 standard; protein; 231 AA.  
DE Respiratory disease differentially expressed protein #65.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP. 34.5%; Score 480.5; DB 8; Length 231;  
Query Match 34.5%; Score 480.5; DB 8; Length 231;  
Best Local Similarity 38.7%; Pred. No. 1.4e-45;  
RESULT 693  
ID AAE05342 standard; protein; 238 AA.  
DE Mouse secreted protein #1.  
PN WO200148192-A1.  
PD 05-JUL-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD. 34.4%; Score 479.5; DB 4; Length 238;  
Query Match 34.4%; Score 479.5; DB 4; Length 238;  
Best Local Similarity 37.3%; Pred. No. 1.9e-45;  
RESULT 694  
ID ABO00865 standard; protein; 246 AA.  
DE Polypeptide encoded by novel human contig #116.



PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC. 33.2%; Score 461.5; DB 6; Length 246;  
Query Match 39.3%; Pred. No. 2.2e-43;  
Best Local Similarity  
RESULT 695  
ID ABB60356 standard; protein; 246 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7860.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 26.0%; Score 361.5; DB 4; Length 246;  
Query Match 33.6%; Pred. No. 4.9e-32;  
Best Local Similarity  
RESULT 696  
ID AAY36219 standard; protein; 69 AA.  
DE Human secreted protein #91.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET.  
Query Match 25.7%; Score 358; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
RESULT 697  
ID AAY36172 standard; protein; 69 AA.  
DE Human secreted protein #44.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET.  
Query Match 25.7%; Score 358; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
RESULT 698  
ID ADJ46071 standard; protein; 69 AA.  
DE Novel human secreted protein-related protein sequence SeqID224.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 25.7%; Score 358; DB 7; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
RESULT 699  
ID ADJ45977 standard; protein; 69 AA.  
DE Novel human secreted protein-related protein sequence SeqID130.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 25.7%; Score 358; DB 7; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
RESULT 700  
ID ADP19480 standard; protein; 69 AA.  
DE Human secreted polypeptide #331.  
PN US2004110939-A1.  
PD 10-JUN-2004.  
PA (GEST ) GENSET SA.  
Query Match 25.7%; Score 358; DB 8; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.1e-32;  
RESULT 701  
ID ABG28122 standard; protein; 200 AA.  
DE Novel human diagnostic protein #28113.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. 25.6%; Score 356.5; DB 4; Length 200;  
Query Match 74.0%; Pred. No. 1.4e-31;  
Best Local Similarity  
RESULT 702  
ID ABB97776 standard; protein; 85 AA.  
DE Human secretory polypeptide (SPTM) 28.  
PN WO200220756-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC. 25.6%; Score 356; DB 5; Length 85;  
Query Match 86.1%; Pred. No. 4.8e-32;  
Best Local Similarity

RESULT 703  
ID AAY04148 standard; protein; 69 AA.  
DE Human 5' EST secreted protein SEQ ID NO:19.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 704  
ID AAW93616 standard; protein; 69 AA.  
DE Human 5' EST secreted protein clone 58-34-2-E7-FL2.  
PN WO9906551-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 705  
ID AAY04166 standard; protein; 69 AA.  
DE Human 5' EST secreted protein SEQ ID NO:19.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 706  
ID AAY35882 standard; protein; 69 AA.  
DE Extended human secreted protein sequence, SEQ ID NO. 19.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 707  
ID AAY59645 standard; protein; 69 AA.  
DE Secreted protein extended EST protein sequence #2.  
PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 708  
ID AAY01590 standard; protein; 69 AA.  
DE Secreted protein encoded by an extended 5' EST cDNA sequence.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 709  
ID AAY12982 standard; protein; 69 AA.  
DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 710  
ID AAY25451 standard; protein; 69 AA.  
DE Human secreted protein 2 derived from extended cDNA.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 711  
ID AAY12672 standard; peptide; 69 AA.  
DE Human 5' EST secreted protein.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 712  
ID AAY12672 standard; peptide; 69 AA.  
DE Human 5' EST secreted protein.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 2; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 712

ID AAG00010 standard; protein; 69 AA.  
DE Human secreted protein #1.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Query Match 25.3%; Score 352; DB 3; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 713  
ID ADU73027 standard; protein; 69 AA.  
DE cDNA 58-34-2-E7-FL2-encoded secreted protein, SEQ ID NO:1.  
PN US6822072-B1.  
PD 23-NOV-2004.  
PA (GEST ) GENSET SA.  
Query Match 25.3%; Score 352; DB 8; Length 69;  
Best Local Similarity 98.5%; Pred. No. 1e-31;  
RESULT 714  
ID ABB89768 standard; protein; 180 AA.  
DE Human polypeptide SEQ ID NO 2144.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 22.8%; Score 317.5; DB 5; Length 180;  
Best Local Similarity 33.3%; Pred. No. 3.2e-27;  
RESULT 715  
ID AAG81279 standard; protein; 114 AA.  
DE Human AFP protein sequence SEQ ID NO:76.  
PN WO200129221-A2.  
PD 26-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 19.6%; Score 272.5; DB 4; Length 114;  
Best Local Similarity 47.5%; Pred. No. 2.2e-22;  
RESULT 716  
ID AAB93632 standard; protein; 132 AA.  
DE Human protein sequence SEQ ID NO:13115.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 18.0%; Score 251; DB 4; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 717  
ID ADL06520 standard; protein; 132 AA.  
DE Human tumour-associated antigenic target (TAT) polypeptide #19.  
PN WO2004016225-A2.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 18.0%; Score 251; DB 8; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 718  
ID ADJ75472 standard; protein; 132 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:724.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 18.0%; Score 251; DB 8; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 719  
ID ADR14452 standard; protein; 132 AA.  
DE Human NF-kappaB pathway-associated protein SeqID453.  
PN WO2004065577-A2.  
PD 05-AUG-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 18.0%; Score 251; DB 8; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 720  
ID ADP24981 standard; protein; 132 AA.  
DE PRO polypeptide SEQ ID NO:2159.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 18.0%; Score 251; DB 8; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 721  
ID ADU06610 standard; protein; 132 AA.

DE Novel bronchial cancer-associated human protein SeqID836.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTANOS-VELEZ E.  
Query Match 18.0%; Score 251; DB 8; Length 132;  
Best Local Similarity 33.3%; Pred. No. 7.4e-20;  
RESULT 722  
ID ADS11008 standard; protein; 233 AA.  
DE Human therapeutic protein - SEQ ID 1245.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 15.8%; Score 220.5; DB 8; Length 233;  
Best Local Similarity 27.2%; Pred. No. 4.7e-16;  
RESULT 723  
ID ABO00507 standard; protein; 283 AA.  
DE Novel human polypeptide #94.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.4%; Score 214.5; DB 6; Length 283;  
Best Local Similarity 26.2%; Pred. No. 3e-15;  
RESULT 724  
ID AAB08866 standard; protein; 249 AA.  
DE Amino acid sequence of a human secretory protein.  
PN WO200052151-A2.  
PD 08-SEP-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 15.2%; Score 212; DB 3; Length 249;  
Best Local Similarity 26.5%; Pred. No. 4.8e-15;  
RESULT 725  
ID AAM38964 standard; protein; 249 AA.  
DE Human polypeptide SEQ ID NO 2109.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.2%; Score 212; DB 4; Length 249;  
Best Local Similarity 26.5%; Pred. No. 4.8e-15;  
RESULT 726  
ID AAM51628 standard; protein; 249 AA.  
DE Human plasminogen activator inhibitor 2-27 polypeptide.  
PN CN1313331-A.  
PD 19-SEP-2001.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 15.2%; Score 212; DB 5; Length 249;  
Best Local Similarity 26.5%; Pred. No. 4.8e-15;  
RESULT 727  
ID ADP18677 standard; protein; 249 AA.  
DE Human protein encoded by TAT414 cDNA used to treat cancer SeqID 37.  
PN WO2004045516-A2.  
PD 03-JUN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 15.2%; Score 212; DB 8; Length 249;  
Best Local Similarity 26.5%; Pred. No. 4.8e-15;  
RESULT 728  
ID AAY12179 standard; protein; 36 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 492.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 14.0%; Score 195; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-14;  
RESULT 729  
ID AAM40750 standard; protein; 274 AA.  
DE Human polypeptide SEQ ID NO 5681.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 192.5; DB 4; Length 274;  
Best Local Similarity 31.4%; Pred. No. 9e-13;  
RESULT 730

ID ABG17213 standard; protein; 308 AA.  
DE Novel human diagnostic protein #17204.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.9%; Score 180; DB 4; Length 308;  
Best Local Similarity 100.0%; Pred. No. 2.8e-11;  
RESULT 731  
ID ABG16460 standard; protein; 466 AA.  
DE Novel human diagnostic protein #16451.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.7%; Score 176.5; DB 4; Length 466;  
Best Local Similarity 60.0%; Pred. No. 1.2e-10;  
RESULT 732  
ID AAE00332 standard; protein; 253 AA.  
DE Human membrane-bound protein-60 alternative mature protein sequence.  
PN WO200123567-A1.  
PD 05-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 11.5%; Score 160.5; DB 4; Length 253;  
Best Local Similarity 24.5%; Pred. No. 3.5e-09;  
RESULT 733  
ID AAE00331 standard; protein; 256 AA.  
DE Human membrane-bound protein-60 (Zsig60) mature protein sequence.  
PN WO200123567-A1.  
PD 05-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 11.5%; Score 160.5; DB 4; Length 256;  
Best Local Similarity 24.5%; Pred. No. 3.5e-09;  
RESULT 734  
ID AAB18985 standard; protein; 271 AA.  
DE Amino acid sequence of a human transmembrane protein.  
PN WO200056891-A2.  
PD 28-SEP-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 11.5%; Score 160.5; DB 3; Length 271;  
Best Local Similarity 24.5%; Pred. No. 3.8e-09;  
RESULT 735  
ID AAE00330 standard; protein; 271 AA.  
DE Human membrane-bound protein-60 (Zsig60).  
PN WO200123567-A1.  
PD 05-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 11.5%; Score 160.5; DB 4; Length 271;  
Best Local Similarity 24.5%; Pred. No. 3.8e-09;  
RESULT 736  
ID AAY48244 standard; protein; 304 AA.  
DE Human prostate cancer-associated protein 30.  
PN DE19811193-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 10.9%; Score 152; DB 2; Length 304;  
Best Local Similarity 24.0%; Pred. No. 4.1e-08;  
RESULT 737  
ID AAE00334 standard; protein; 160 AA.  
DE Human membrane-bound protein-60 alternative mature extracellular portion.  
PN WO200123567-A1.  
PD 05-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 10.9%; Score 151.5; DB 4; Length 160;  
Best Local Similarity 29.5%; Pred. No. 1.9e-08;  
RESULT 738  
ID AAE00333 standard; protein; 163 AA.  
DE Human membrane-bound protein-60 (Zsig60) mature extracellular portion.  
PN WO200123567-A1.  
PD 05-APR-2001.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 10.9%; Score 151.5; DB 4; Length 163;  
Best Local Similarity 29.5%; Pred. No. 2e-08;  
RESULT 739  
ID AAY94930 standard; protein; 437 AA.

DE Human secreted protein clone qal36\_1 protein sequence SEQ ID NO:66.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEMY ) GENETICS INST INC.  
Query Match 10.9%; Score 151.5; DB 3; Length 437;  
Best Local Similarity 26.8%; Pred. No. 7.7e-08;  
RESULT 740  
ID AAY95013 standard; protein; 178 AA.  
DE Human secreted protein vc48\_1, SEQ ID NO:66.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 10.6%; Score 147.5; DB 3; Length 178;  
Best Local Similarity 24.9%; Pred. No. 6.4e-08;  
RESULT 741  
ID ADN02727 standard; protein; 255 AA.  
DE Human receptor and membrane -associated protein #30.  
PN WO2004029218-A2.  
PD 08-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 10.5%; Score 146.5; DB 8; Length 255;  
Best Local Similarity 24.6%; Pred. No. 1.4e-07;  
RESULT 742  
ID ABO00615 standard; protein; 63 AA.  
DE Novel human polypeptide #202.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.1%; Score 126; DB 6; Length 63;  
Best Local Similarity 47.2%; Pred. No. 4.2e-06;  
RESULT 743  
ID ADS11007 standard; protein; 127 AA.  
DE Human therapeutic protein - SEQ ID 1244.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 8.8%; Score 122.5; DB 8; Length 127;  
Best Local Similarity 32.1%; Pred. No. 2.8e-05;  
RESULT 744  
ID AAY04149 standard; peptide; 21 AA.  
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 745  
ID AAY11369 standard; protein; 21 AA.  
DE Human 5' EST secreted protein SEQ ID NO:20.  
PN WO9906551-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 746  
ID AAY12516 standard; peptide; 21 AA.  
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.  
PN WO9906553-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 747  
ID AAY35883 standard; peptide; 21 AA.  
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 748  
ID AAY59644 standard; peptide; 21 AA.  
DE Secreted protein extended EST signal peptide #2.

PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 749  
ID AAY25452 standard; peptide; 21 AA.  
DE Human secreted protein 2 signal peptide derived from extended cDNA.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 750  
ID AAY12671 standard; peptide; 21 AA.  
DE Human 5' EST secreted protein signal peptide.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 751  
ID AAY11711 standard; protein; 21 AA.  
DE Peptide encoded by extended cDNA derived from 5' EST.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 752  
ID AAY64644 standard; peptide; 21 AA.  
DE Human 58-34-2-E7-FL2 signal peptide.  
PN WO9953051-A2.  
PD 21-OCT-1999.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 753  
ID AAG00011 standard; peptide; 21 AA.  
DE Human secreted protein #1 signal peptide.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 754  
ID AAO20328 standard; peptide; 21 AA.  
DE Signal peptide encoded by the cDNA 58-34-2-E7-FL2.  
PN CA2343602-A1.  
PD 18-OCT-2001.  
PA (GEST ) GENSET.  
Query Match 8.5%; Score 118; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 755  
ID ADJ45867 standard; peptide; 21 AA.  
DE Novel human secreted protein-related peptide sequence SeqID20.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 8.5%; Score 118; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 756  
ID ADM77739 standard; peptide; 21 AA.  
DE Signal sequence #2.  
PN US2003162176-A1.  
PD 28-AUG-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 8.5%; Score 118; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 757  
ID ADU71405 standard; peptide; 21 AA.  
DE cDNA 58-34-2-E7-FL2-encoded secretory signal peptide, SEQ ID NO:2.  
PN US6822072-B1.  
PD 23-NOV-2004.  
PA (GEST ) GENSET SA.  
Query Match 8.5%; Score 118; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 758  
ID ADZ89199 standard; peptide; 21 AA.  
DE Signal peptide from secreted protein encoded by extended EST cDNA #2.  
PN US2005106599-A1.  
PD 19-MAY-2005.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 8.5%; Score 118; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 759  
ID ADZ72396 standard; peptide; 21 AA.  
DE Human 5' EST encoded signal peptide SEQ ID NO:2.  
PN US2005106595-A1.  
PD 19-MAY-2005.  
PA (GEST ) GENSET SA.  
Query Match 8.5%; Score 118; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 760  
ID AAY04167 standard; peptide; 21 AA.  
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.1%; Score 113; DB 2; Length 21;  
Best Local Similarity 95.2%; Pred. No. 2.8e-05;  
RESULT 761  
ID AAU04087 standard; peptide; 21 AA.  
DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.  
PN EP1104808-A1.  
PD 06-JUN-2001.  
PA (GEST ) GENSET.  
Query Match 8.1%; Score 113; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 762  
ID ABB60233 standard; protein; 275 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7491.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.7%; Score 106.5; DB 4; Length 275;  
Best Local Similarity 21.3%; Pred. No. 0.0053;  
RESULT 763  
ID AAB38499 standard; peptide; 220 AA.  
DE Fragment of human secreted protein encoded by gene 53 clone HFABG18.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.5%; Score 105; DB 3; Length 220;  
Best Local Similarity 22.8%; Pred. No. 0.0057;  
RESULT 764  
ID AAM93195 standard; protein; 218 AA.  
DE Human polypeptide, SEQ ID NO: 2575.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.3%; Score 101; DB 4; Length 218;  
Best Local Similarity 22.8%; Pred. No. 0.016;  
RESULT 765  
ID ADL30542 standard; protein; 218 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 2575.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.3%; Score 101; DB 8; Length 218;

RESULT 757  
ID ADU71405 standard; peptide; 21 AA.  
DE cDNA 58-34-2-E7-FL2-encoded secretory signal peptide, SEQ ID NO:2.  
PN US6822072-B1.  
PD 23-NOV-2004.  
PA (GEST ) GENSET SA.  
Query Match 8.5%; Score 118; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 758  
ID ADZ89199 standard; peptide; 21 AA.  
DE Signal peptide from secreted protein encoded by extended EST cDNA #2.  
PN US2005106599-A1.  
PD 19-MAY-2005.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
Query Match 8.5%; Score 118; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 759  
ID ADZ72396 standard; peptide; 21 AA.  
DE Human 5' EST encoded signal peptide SEQ ID NO:2.  
PN US2005106595-A1.  
PD 19-MAY-2005.  
PA (GEST ) GENSET SA.  
Query Match 8.5%; Score 118; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
RESULT 760  
ID AAY04167 standard; peptide; 21 AA.  
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 8.1%; Score 113; DB 2; Length 21;  
Best Local Similarity 95.2%; Pred. No. 2.8e-05;  
RESULT 761  
ID AAU04087 standard; peptide; 21 AA.  
DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.  
PN EP1104808-A1.  
PD 06-JUN-2001.  
PA (GEST ) GENSET.  
Query Match 8.1%; Score 113; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
RESULT 762  
ID ABB60233 standard; protein; 275 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 7491.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.7%; Score 106.5; DB 4; Length 275;  
Best Local Similarity 21.3%; Pred. No. 0.0053;  
RESULT 763  
ID AAB38499 standard; peptide; 220 AA.  
DE Fragment of human secreted protein encoded by gene 53 clone HFABG18.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.5%; Score 105; DB 3; Length 220;  
Best Local Similarity 22.8%; Pred. No. 0.0057;  
RESULT 764  
ID AAM93195 standard; protein; 218 AA.  
DE Human polypeptide, SEQ ID NO: 2575.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 7.3%; Score 101; DB 4; Length 218;  
Best Local Similarity 22.8%; Pred. No. 0.016;  
RESULT 765  
ID ADL30542 standard; protein; 218 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 2575.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.3%; Score 101; DB 8; Length 218;

Best Local Similarity 22.8%; Pred. No. 0.016;  
RESULT 766  
ID AEB38816 standard; protein; 581 AA.  
DE L. pneumophila protein SEQ ID NO 3148.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 7.1%; Score 99.5; DB 9; Length 581;  
Best Local Similarity 24.4%; Pred. No. 0.092;  
RESULT 767  
ID ADM06102 standard; protein; 187 AA.  
DE Human protein of the invention SEQ ID NO:4787.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.1%; Score 99; DB 7; Length 187;  
Best Local Similarity 23.4%; Pred. No. 0.022;  
RESULT 768  
ID AEC89032 standard; protein; 187 AA.  
DE Human cDNA clone protein TRACH20128110, SEQ ID 4787.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 7.1%; Score 99; DB 9; Length 187;  
Best Local Similarity 23.4%; Pred. No. 0.022;  
RESULT 769  
ID ABU45347 standard; protein; 1066 AA.  
DE Protein encoded by Prokaryotic essential gene #30874.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.1%; Score 98.5; DB 6; Length 1066;  
Best Local Similarity 19.5%; Pred. No. 0.28;  
RESULT 770  
ID ABU47563 standard; protein; 1120 AA.  
DE Protein encoded by Prokaryotic essential gene #33090.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.1%; Score 98.5; DB 6; Length 1120;  
Best Local Similarity 19.5%; Pred. No. 0.3;  
RESULT 771  
ID ABU46980 standard; protein; 1120 AA.  
DE Protein encoded by Prokaryotic essential gene #32507.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.1%; Score 98.5; DB 6; Length 1120;  
Best Local Similarity 19.5%; Pred. No. 0.3;  
RESULT 772  
ID AEB42187 standard; protein; 268 AA.  
DE L. pneumophila protein SEQ ID NO 6519.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.8%; Score 94.5; DB 9; Length 268;  
Best Local Similarity 22.6%; Pred. No. 0.12;  
RESULT 773  
ID AEB39048 standard; protein; 291 AA.  
DE L. pneumophila protein SEQ ID NO 3380.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.8%; Score 94.5; DB 9; Length 291;  
Best Local Similarity 22.6%; Pred. No. 0.12;

Best Local Similarity 22.6%; Pred. No. 0.13;  
RESULT 774  
ID ABU34113 standard; protein; 548 AA.  
DE Protein encoded by Prokaryotic essential gene #19640.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.8%; Score 94.5; DB 6; Length 548;  
Best Local Similarity 18.2%; Pred. No. 0.31;  
RESULT 775  
ID ABU39811 standard; protein; 269 AA.  
DE Protein encoded by Prokaryotic essential gene #25338.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.8%; Score 94; DB 6; Length 269;  
Best Local Similarity 21.7%; Pred. No. 0.13;  
RESULT 776  
ID AEC57250 standard; protein; 452 AA.  
DE L. acidophilus maltose ABC transporter permease SEQ ID 64.  
PN WO2005084411-A2.  
PD 15-SEP-2005.  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
Query Match 6.8%; Score 94; DB 9; Length 452;  
Best Local Similarity 19.2%; Pred. No. 0.27;  
RESULT 777  
ID AAG44537 standard; protein; 303 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55801.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 93.5; DB 3; Length 303;  
Best Local Similarity 21.8%; Pred. No. 0.18;  
RESULT 778  
ID AAG44536 standard; protein; 367 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55800.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 93.5; DB 3; Length 367;  
Best Local Similarity 21.8%; Pred. No. 0.24;  
RESULT 779  
ID ABU15091 standard; protein; 1120 AA.  
DE Protein encoded by Prokaryotic essential gene #618.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 93; DB 6; Length 1120;  
Best Local Similarity 19.6%; Pred. No. 1.2;  
RESULT 780  
ID ABU47616 standard; protein; 473 AA.  
DE Protein encoded by Prokaryotic essential gene #33143.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.6%; Score 92.5; DB 6; Length 473;  
Best Local Similarity 22.8%; Pred. No. 0.43;  
RESULT 781  
ID ABB89477 standard; protein; 118 AA.  
DE Human polypeptide SEQ ID NO 1853.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.6%; Score 91.5; DB 5; Length 118;  
Best Local Similarity 28.0%; Pred. No. 0.083;  
RESULT 782  
ID ADC94520 standard; protein; 291 AA.  
DE E. faecium protein sequence SEQ ID 4147.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.6%; Score 91.5; DB 7; Length 291;  
Best Local Similarity 22.9%; Pred. No. 0.29;  
RESULT 783  
ID ADN23444 standard; protein; 373 AA.



DE Bacterial polypeptide #6097.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.6%; Score 91.5; DB 8; Length 373;  
Best Local Similarity 23.0%; Pred. No. 0.41;  
RESULT 784  
ID AAU03808 standard; protein; 387 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.  
PN WO200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA ) PHARMACIA & UPJOHN.  
Query Match 6.6%; Score 91.5; DB 4; Length 387;  
Best Local Similarity 23.0%; Pred. No. 0.43;  
RESULT 785  
ID ABB91939 standard; protein; 712 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1150.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.6%; Score 91.5; DB 5; Length 712;  
Best Local Similarity 22.2%; Pred. No. 0.99;  
RESULT 786  
ID ADX68404 standard; protein; 486 AA.  
DE Plant full length insert polypeptide seqid 39247.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 6.5%; Score 91; DB 8; Length 486;  
Best Local Similarity 22.6%; Pred. No. 0.67;  
RESULT 787  
ID ADX87645 standard; protein; 486 AA.  
DE Plant full length insert polypeptide seqid 50309.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 6.5%; Score 91; DB 8; Length 486;  
Best Local Similarity 22.6%; Pred. No. 0.67;  
RESULT 788  
ID ADY12322 standard; protein; 487 AA.  
DE Plant full length insert polypeptide seqid 68137.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 6.5%; Score 91; DB 8; Length 487;  
Best Local Similarity 22.6%; Pred. No. 0.67;  
RESULT 789  
ID ADN46339 standard; protein; 451 AA.  
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID217.  
PN WO2004022736-A1.  
PD 18-MAR-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 6.5%; Score 90.5; DB 8; Length 451;  
Best Local Similarity 21.2%; Pred. No. 0.68;

RESULT 790  
ID AAB76803 standard; protein; 283 AA.  
DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.  
PN WO200100805-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 6.5%; Score 90; DB 4; Length 283;  
Best Local Similarity 23.8%; Pred. No. 0.41;  
RESULT 791  
ID AAG89779 standard; protein; 283 AA.  
DE C glutamicum protein fragment SEQ ID NO: 3533.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 6.5%; Score 90; DB 4; Length 283;  
Best Local Similarity 23.8%; Pred. No. 0.41;  
RESULT 792  
ID AED46975 standard; protein; 283 AA.  
DE Membrane construction and membrane transport protein SEQ ID 252.  
PN US2005244935-A1.  
PD 03-NOV-2005.  
PA (BADI ) BASF AG.  
Query Match 6.5%; Score 90; DB 9; Length 283;  
Best Local Similarity 23.8%; Pred. No. 0.41;  
RESULT 793  
ID AED46977 standard; protein; 283 AA.  
DE Membrane construction and membrane transport protein SEQ ID 254.  
PN US2005244935-A1.  
PD 03-NOV-2005.  
PA (BADI ) BASF AG.  
Query Match 6.5%; Score 90; DB 9; Length 283;  
Best Local Similarity 23.8%; Pred. No. 0.41;  
RESULT 794  
ID ADP98865 standard; protein; 505 AA.  
DE C. albicans specific gene, orf6.4442, protein sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 6.5%; Score 90; DB 8; Length 505;  
Best Local Similarity 20.5%; Pred. No. 0.91;  
RESULT 795  
ID ABU45537 standard; protein; 458 AA.  
DE Protein encoded by Prokaryotic essential gene #31064.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 89.5; DB 6; Length 458;  
Best Local Similarity 22.8%; Pred. No. 0.91;  
RESULT 796  
ID ABP26393 standard; protein; 579 AA.  
DE Streptococcus polypeptide SEQ ID NO 1962.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.4%; Score 89.5; DB 5; Length 579;  
Best Local Similarity 24.8%; Pred. No. 1.3;  
RESULT 797  
ID ADV88815 standard; protein; 579 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 1209.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.4%; Score 89.5; DB 8; Length 579;  
Best Local Similarity 24.8%; Pred. No. 1.3;  
RESULT 798  
ID ADV82204 standard; protein; 579 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3345.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.

PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.4%; Score 89.5; DB 8; Length 579;  
Best Local Similarity 24.8%; Pred. No. 1.3;  
RESULT 799  
ID ADV80068 standard; protein; 579 AA.  
DE Streptococcus agalactiae protein, SEQ ID 1209.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.4%; Score 89.5; DB 8; Length 579;  
Best Local Similarity 24.8%; Pred. No. 1.3;  
RESULT 800  
ID ABU50406 standard; protein; 428 AA.  
DE Protein encoded by Prokaryotic essential gene #35933.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 89; DB 6; Length 428;  
Best Local Similarity 21.6%; Pred. No. 0.94;  
RESULT 801  
ID AAB94689 standard; protein; 637 AA.  
DE Human protein sequence SEQ ID NO:15654.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.4%; Score 89; DB 4; Length 637;  
Best Local Similarity 21.5%; Pred. No. 1.6;  
RESULT 802  
ID ABU23408 standard; protein; 642 AA.  
DE Protein encoded by Prokaryotic essential gene #8935.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 89; DB 6; Length 642;  
Best Local Similarity 20.8%; Pred. No. 1.6;  
RESULT 803  
ID AAU03497 standard; protein; 757 AA.  
DE Human sterol sensing domain protein.  
PN WO200146227-A2.  
PD 28-JUN-2001.  
PA (UYZU-) UNIV ZURICH.  
Query Match 6.4%; Score 89; DB 4; Length 757;  
Best Local Similarity 21.5%; Pred. No. 2.1;  
RESULT 804  
ID AAB41293 standard; protein; 758 AA.  
DE Human ORFX ORF1057 polypeptide sequence SEQ ID NO:2114.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.4%; Score 89; DB 3; Length 758;  
Best Local Similarity 21.5%; Pred. No. 2.1;  
RESULT 805  
ID AAU74820 standard; protein; 1124 AA.  
DE Human REPTR 3 protein.  
PN WO200198354-A2.  
PD 27-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.4%; Score 89; DB 5; Length 1124;  
Best Local Similarity 21.5%; Pred. No. 3.6;  
RESULT 806  
ID ADA55083 standard; protein; 1203 AA.  
DE Human protein, SEQ ID 2651.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.4%; Score 89; DB 6; Length 1203;  
Best Local Similarity 21.5%; Pred. No. 3.9;  
RESULT 807  
ID ABG31547 standard; protein; 1330 AA.  
DE Human patched-like protein.  
PN WO200246402-A2.

PD 13-JUN-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.4%; Score 89; DB 5; Length 1330;  
Best Local Similarity 21.5%; Pred. No. 4.5;  
RESULT 808  
ID AEB40780 standard; protein; 361 AA.  
DE L. pneumophila protein SEQ ID NO 5112.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.4%; Score 88.5; DB 9; Length 361;  
Best Local Similarity 20.9%; Pred. No. 0.85;  
RESULT 809  
ID ADY10982 standard; protein; 372 AA.  
DE Plant full length insert polypeptide seqid 66797.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 6.4%; Score 88.5; DB 8; Length 372;  
Best Local Similarity 19.3%; Pred. No. 0.89;  
RESULT 810  
ID AEB37466 standard; protein; 374 AA.  
DE L. pneumophila protein SEQ ID NO 1798.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.4%; Score 88.5; DB 9; Length 374;  
Best Local Similarity 20.9%; Pred. No. 0.89;  
RESULT 811  
ID AAB96747 standard; protein; 430 AA.  
DE Putative P. abyssi permease #26.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 6.4%; Score 88.5; DB 4; Length 430;  
Best Local Similarity 23.8%; Pred. No. 1.1;  
RESULT 812  
ID AAR37309 standard; protein; 1165 AA.  
DE Cardiac adenylyl cyclase.  
PN EP543137-A1.  
PD 26-MAY-1993.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Query Match 6.3%; Score 88; DB 2; Length 1165;  
Best Local Similarity 20.5%; Pred. No. 4.9;  
RESULT 813  
ID ABU19097 standard; protein; 233 AA.  
DE Protein encoded by Prokaryotic essential gene #4624.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.3%; Score 87.5; DB 6; Length 233;  
Best Local Similarity 22.8%; Pred. No. 0.6;  
RESULT 814  
ID ADD67113 standard; protein; 322 AA.  
DE Homogentisate prenyl transferase.  
PN WO2003080647-A2.  
PD 02-OCT-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match 6.3%; Score 87.5; DB 7; Length 322;  
Best Local Similarity 22.6%; Pred. No. 0.94;  
RESULT 815

ID ADC77581 standard; protein; 453 AA.  
DE Mouse TMS2 amino acid sequence.  
PN WO2003066829-A2.  
PD 14-AUG-2003.  
PA (DISC-) DISCOVERY GENOMICS INC.  
Query Match 6.3%; Score 87.5; DB 7; Length 453;  
Best Local Similarity 19.9%; Pred. No. 1.5;  
RESULT 816  
ID ADS28619 standard; protein; 482 AA.  
DE Bacterial polypeptide #17652.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.3%; Score 87.5; DB 8; Length 482;  
Best Local Similarity 21.2%; Pred. No. 1.6;  
RESULT 817  
ID AEB38041 standard; protein; 521 AA.  
DE L. pneumophila protein SEQ ID NO 2373.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 87.5; DB 9; Length 521;  
Best Local Similarity 22.5%; Pred. No. 1.8;  
RESULT 818  
ID AEB41335 standard; protein; 521 AA.  
DE L. pneumophila protein SEQ ID NO 5667.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 87.5; DB 9; Length 521;  
Best Local Similarity 22.5%; Pred. No. 1.8;  
RESULT 819  
ID AEB41995 standard; protein; 535 AA.  
DE L. pneumophila protein SEQ ID NO 6327.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.2%; Score 87; DB 9; Length 535;  
Best Local Similarity 26.0%; Pred. No. 2.2;  
RESULT 820  
ID ABU33543 standard; protein; 239 AA.  
DE Protein encoded by Prokaryotic essential gene #19070.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 86.5; DB 6; Length 239;  
Best Local Similarity 20.4%; Pred. No. 0.81;  
RESULT 821  
ID ADT05661 standard; protein; 261 AA.  
DE Haemophilus influenzae (NTHi) protein - SEQ ID 697.  
PN WO2004078949-A2.  
PD 16-SEP-2004.  
PA (CHIL-) CHILDRENS HOSPITAL INC.  
Query Match 6.2%; Score 86.5; DB 8; Length 261;  
Best Local Similarity 24.2%; Pred. No. 0.92;  
RESULT 822  
ID ADH87029 standard; protein; 356 AA.  
DE Enterococcus faecalis polypeptide #1509.  
PN US6617156-B1.  
PD 09-SEP-2003.

PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.2%; Score 86.5; DB 7; Length 356;  
Best Local Similarity 19.2%; Pred. No. 1.4;  
RESULT 823  
ID ADS44642 standard; protein; 400 AA.  
DE Bacterial polypeptide #23072.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.2%; Score 86.5; DB 8; Length 400;  
Best Local Similarity 21.9%; Pred. No. 1.7;  
RESULT 824  
ID ABB47717 standard; protein; 583 AA.  
DE Listeria monocytogenes protein #421.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 6.2%; Score 86.5; DB 5; Length 583;  
Best Local Similarity 19.4%; Pred. No. 2.8;  
RESULT 825  
ID AAG39112 standard; protein; 1346 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 86.5; DB 3; Length 1346;  
Best Local Similarity 18.2%; Pred. No. 8.8;  
RESULT 826  
ID AAG39111 standard; protein; 1390 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 86.5; DB 3; Length 1390;  
Best Local Similarity 18.2%; Pred. No. 9.2;  
RESULT 827  
ID AAG39110 standard; protein; 1403 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.2%; Score 86.5; DB 3; Length 1403;  
Best Local Similarity 18.2%; Pred. No. 9.3;  
RESULT 828  
ID ABM73219 standard; protein; 372 AA.  
DE Staphylococcus aureus protein #2459.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.2%; Score 86; DB 6; Length 372;  
Best Local Similarity 18.1%; Pred. No. 1.7;  
RESULT 829  
ID AAG98347 standard; protein; 396 AA.  
DE Escherichia coli protein sequence SEQ ID NO:395.  
PN WO200148209-A2.  
PD 05-JUL-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 86; DB 4; Length 396;  
Best Local Similarity 21.9%; Pred. No. 1.9;  
RESULT 830  
ID ABU14798 standard; protein; 396 AA.  
DE Protein encoded by Prokaryotic essential gene #325.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 86; DB 6; Length 396;  
Best Local Similarity 21.9%; Pred. No. 1.9;  
RESULT 831  
ID ABB90798 standard; protein; 725 AA.  
DE Herbicidally active polypeptide SEQ ID NO 9.  
PN WO200210210-A2.

PD 07-FEB-2002.  
PA (FARB ) BAYER AG. 6.2%; Score 86; DB 5; Length 725;  
Query Match 18.9%; Pred. No. 4.3;  
Best Local Similarity  
RESULT 832  
ID AAB11039 standard; protein; 841 AA.  
DE S. xylosum mprF protein.  
PN DE19914817-A1.  
PD 05-OCT-2000.  
PA (PETR-) PETRY GENMEDICS GMBH. 6.2%; Score 86; DB 3; Length 841;  
Query Match 18.3%; Pred. No. 5.2;  
Best Local Similarity  
RESULT 833  
ID ABP77912 standard; protein; 295 AA.  
DE N. Gonorrhoeae amino acid sequence SEQ ID 2354.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA. 6.1%; Score 85.5; DB 6; Length 295;  
Query Match 21.6%; Pred. No. 1.4;  
Best Local Similarity  
RESULT 834  
ID ABU37235 standard; protein; 295 AA.  
DE Protein encoded by Prokaryotic essential gene #22762.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 6.1%; Score 85.5; DB 6; Length 295;  
Query Match 21.6%; Pred. No. 1.4;  
Best Local Similarity  
RESULT 835  
ID ABJ39122 standard; protein; 311 AA.  
DE Molecule for disease detection and treatment (MDDT)-32 protein sequence.  
PN WO2003052049-A2.  
PD 26-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC. 6.1%; Score 85.5; DB 6; Length 311;  
Query Match 21.7%; Pred. No. 1.5;  
Best Local Similarity  
RESULT 836  
ID ADC37363 standard; protein; 311 AA.  
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.  
PN WO2003048202-A2.  
PD 12-JUN-2003.  
PA (ASAH ) ASahi KASEI KK. 6.1%; Score 85.5; DB 7; Length 311;  
Query Match 21.7%; Pred. No. 1.5;  
Best Local Similarity  
RESULT 837  
ID ADR58959 standard; protein; 311 AA.  
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 62.  
PN WO2004072277-A2.  
PD 26-AUG-2004.  
PA (ASAH-) ASahi KASEI PHARMA CORP. 6.1%; Score 85.5; DB 8; Length 311;  
Query Match 21.7%; Pred. No. 1.5;  
Best Local Similarity  
RESULT 838  
ID ADU76431 standard; protein; 311 AA.  
DE Progesterin-YOLO02c-CGI-45 receptor, INTP047.  
PN WO2004101618-A2.  
PD 25-NOV-2004.  
PA (INPH-) INPHARMATICA LTD. 6.1%; Score 85.5; DB 8; Length 311;  
Query Match 21.7%; Pred. No. 1.5;  
Best Local Similarity  
RESULT 839  
ID AAM93524 standard; protein; 329 AA.  
DE Human polypeptide, SEQ ID NO: 3257.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST. 6.1%; Score 85.5; DB 4; Length 329;  
Query Match 23.0%; Pred. No. 1.6;  
Best Local Similarity  
RESULT 840  
ID AAB92687 standard; protein; 329 AA.  
DE Human protein sequence SEQ ID NO:11071.  
PN EPI074617-A2.  
PD 07-FEB-2001.

PA (HELI-) HELIX RES INST. 6.1%; Score 85.5; DB 4; Length 329;  
Query Match 23.0%; Pred. No. 1.6;  
Best Local Similarity  
RESULT 841  
ID ADL31224 standard; protein; 329 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3257.  
PN EPI396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. 6.1%; Score 85.5; DB 8; Length 329;  
Query Match 23.0%; Pred. No. 1.6;  
Best Local Similarity  
RESULT 842  
ID ADA98171 standard; protein; 359 AA.  
DE Human secreted protein sequence #12.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 6; Length 359;  
Query Match 23.0%; Pred. No. 1.8;  
Best Local Similarity  
RESULT 843  
ID ADA44024 standard; protein; 359 AA.  
DE Human secreted protein SEQ ID 212.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 6; Length 359;  
Query Match 23.0%; Pred. No. 1.8;  
Best Local Similarity  
RESULT 844  
ID ADC20341 standard; protein; 359 AA.  
DE Human secreted protein - amino acid sequence #17.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 7; Length 359;  
Query Match 23.0%; Pred. No. 1.8;  
Best Local Similarity  
RESULT 845  
ID ADF10683 standard; protein; 359 AA.  
DE Human secreted protein #5.  
PN WO200299085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 7; Length 359;  
Query Match 23.0%; Pred. No. 1.8;  
Best Local Similarity  
RESULT 846  
ID AAB75546 standard; protein; 360 AA.  
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.  
PN WO200077026-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 4; Length 360;  
Query Match 23.0%; Pred. No. 1.9;  
Best Local Similarity  
RESULT 847  
ID AAW61371 standard; protein; 439 AA.  
DE Non-adrenergic SM binding protein.  
PN EP848059-A1.  
PD 17-JUN-1998.  
PA (VETI-) VETIGEN. 6.1%; Score 85.5; DB 2; Length 439;  
Query Match 23.0%; Pred. No. 2.4;  
Best Local Similarity  
RESULT 848  
ID AAB75598 standard; protein; 530 AA.  
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.  
PN WO200077026-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC. 6.1%; Score 85.5; DB 4; Length 530;  
Query Match 23.0%; Pred. No. 3.2;  
Best Local Similarity  
RESULT 849  
ID AAY94910 standard; protein; 545 AA.  
DE Human secreted protein clone pk366\_7 protein sequence SEQ ID NO:26.  
PN WO200009552-A1.

PD 24-FEB-2000.  
PA (GEMY ) GENETICS INST INC.  
Query Match 6.1%; Score 85.5; DB 3; Length 545;  
Best Local Similarity 23.0%; Pred. No. 3.3;  
RESULT 850  
ID AAB94667 standard; protein; 545 AA.  
DE Human protein sequence SEQ ID NO:15600.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.1%; Score 85.5; DB 4; Length 545;  
Best Local Similarity 23.0%; Pred. No. 3.3;  
RESULT 851  
ID AAY82460 standard; protein; 579 AA.  
DE Human SM-11044-binding receptor protein SEQ ID NO:4.  
PN WO200014266-A1.  
PD 16-MAR-2000.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match 6.1%; Score 85.5; DB 3; Length 579;  
Best Local Similarity 23.0%; Pred. No. 3.6;  
RESULT 852  
ID AAY82459 standard; protein; 582 AA.  
DE Human SM-11044-binding receptor protein SEQ ID NO:2.  
PN WO200014266-A1.  
PD 16-MAR-2000.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match 6.1%; Score 85.5; DB 3; Length 582;  
Best Local Similarity 23.0%; Pred. No. 3.6;  
RESULT 853  
ID ABB69104 standard; protein; 700 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 34104.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.1%; Score 85.5; DB 4; Length 700;  
Best Local Similarity 19.7%; Pred. No. 4.6;  
RESULT 854  
ID AEB15131 standard; protein; 265 AA.  
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID46.  
PN US2005153402-A1.  
PD 14-JUL-2005.  
PA (BADI ) BASF AG.  
Query Match 6.1%; Score 85; DB 9; Length 265;  
Best Local Similarity 24.1%; Pred. No. 1.4;  
RESULT 855  
ID ABU34786 standard; protein; 338 AA.  
DE Protein encoded by Prokaryotic essential gene #20313.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 85; DB 6; Length 338;  
Best Local Similarity 23.1%; Pred. No. 1.9;  
RESULT 856  
ID ABU36544 standard; protein; 338 AA.  
DE Protein encoded by Prokaryotic essential gene #22071.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 85; DB 6; Length 338;  
Best Local Similarity 23.1%; Pred. No. 1.9;  
RESULT 857  
ID AAG90802 standard; protein; 419 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4556.  
PN EPL108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 6.1%; Score 85; DB 4; Length 419;  
Best Local Similarity 24.1%; Pred. No. 2.6;  
RESULT 858  
ID AAE20418 standard; protein; 419 AA.  
DE Corynebacterium glutamicum CHRS protein.  
PN WO200220572-A2.  
PD 14-MAR-2002.

PA (DEGS ) DEGUSSA AG.  
Query Match 6.1%; Score 85; DB 5; Length 419;  
Best Local Similarity 24.1%; Pred. No. 2.6;  
RESULT 859  
ID AEB15129 standard; protein; 419 AA.  
DE C glutamicum metabolic pathway regulatory (MR) protein SeqID44.  
PN US2005153402-A1.  
PD 14-JUL-2005.  
PA (BADI ) BASF AG.  
Query Match 6.1%; Score 85; DB 9; Length 419;  
Best Local Similarity 24.1%; Pred. No. 2.6;  
RESULT 860  
ID ABB55143 standard; protein; 443 AA.  
DE Lactococcus lactis protein ysfC.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.1%; Score 85; DB 5; Length 443;  
Best Local Similarity 24.4%; Pred. No. 2.8;  
RESULT 861  
ID AAU78998 standard; protein; 498 AA.  
DE Mouse Rh type C gene (RHCG) protein.  
PN WO200220719-A2.  
PD 14-MAR-2002.  
PA (NYBL-) NEW YORK BLOOD CENT INC.  
Query Match 6.1%; Score 85; DB 5; Length 498;  
Best Local Similarity 20.2%; Pred. No. 3.3;  
RESULT 862  
ID ADE56874 standard; protein; 1166 AA.  
DE Rat Protein Q03343, SEQ ID NO 2729.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.1%; Score 85; DB 7; Length 1166;  
Best Local Similarity 19.8%; Pred. No. 11;  
RESULT 863  
ID AAB02010 standard; protein; 1180 AA.  
DE Type VI adenyllyl cyclase.  
PN US6107076-A.  
PD 22-AUG-2000.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 6.1%; Score 85; DB 3; Length 1180;  
Best Local Similarity 19.8%; Pred. No. 11;  
RESULT 864  
ID ADH88320 standard; protein; 296 AA.  
DE Enterococcus faecalis polypeptide #2800.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.1%; Score 84.5; DB 7; Length 296;  
Best Local Similarity 25.2%; Pred. No. 1.8;  
RESULT 865  
ID ABM68417 standard; protein; 324 AA.  
DE Photorhabdus luminescens protein sequence #1514.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.1%; Score 84.5; DB 6; Length 324;  
Best Local Similarity 23.8%; Pred. No. 2.1;  
RESULT 866  
ID AAY07771 standard; protein; 356 AA.  
DE Human secreted protein fragment encoded from gene 28.  
PN WO9909155-A1.  
PD 25-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 84.5; DB 2; Length 356;  
Best Local Similarity 19.8%; Pred. No. 2.4;  
RESULT 867  
ID ABG75197 standard; protein; 408 AA.  
DE Wheat homogentisate geranylgeranyl transferase.



PN WO2003082899-A2.  
PD 09-OCT-2003.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 6.1%; Score 84.5; DB 7; Length 408;  
Best Local Similarity 25.3%; Pred. No. 2.9;  
RESULT 868  
ID AAG46717 standard; protein; 446 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 84.5; DB 3; Length 446;  
Best Local Similarity 19.0%; Pred. No. 3.2;  
RESULT 869  
ID AAY95015 standard; protein; 453 AA.  
DE Human secreted protein vc61\_1, SEQ ID NO:70.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGEN INC.  
Query Match 6.1%; Score 84.5; DB 3; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 870  
ID AAG65236 standard; protein; 453 AA.  
DE Protein tyrosine kinase 50.  
PN CN1298944-A.  
PD 13-JUN-2001.  
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.  
Query Match 6.1%; Score 84.5; DB 4; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 871  
ID AAU29065 standard; protein; 453 AA.  
DE Human PRO polypeptide sequence #42.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 4; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 872  
ID AAM39489 standard; protein; 453 AA.  
DE Human polypeptide SEQ ID NO 2634.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 84.5; DB 4; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 873  
ID AAB65170 standard; protein; 453 AA.  
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 4; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 874  
ID ABB90299 standard; protein; 453 AA.  
DE Human polypeptide SEQ ID NO 2675.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 84.5; DB 5; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 875  
ID ABU58441 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 876  
ID ABU87989 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 877  
ID ABU84304 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 878  
ID ABR66178 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 879  
ID ABR65568 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 880  
ID ABU99508 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 881  
ID ABU57985 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 882  
ID ABU59063 standard; protein; 453 AA.  
DE Novel human secreted or transmembrane protein PRO732.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 883  
ID ABU82575 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 884  
ID ABU82747 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 885  
ID ABU89868 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 886  
ID ABR68117 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 887

ID ABU60494 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, #24.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 888  
ID ABU96170 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 889  
ID ABU92601 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 890  
ID ABO08678 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 891  
ID ABO02730 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 892  
ID ABR74884 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 893  
ID ABR94646 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 894  
ID ABU13876 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 895  
ID ABU85619 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 896  
ID ABU98779 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 897

ID ABU97994 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 898  
ID ABU91700 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 899  
ID ABU89393 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 900  
ID ABU86234 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 901  
ID ABU67447 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 902  
ID ABU80475 standard; protein; 453 AA.  
DE Human PRO protein #42.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 903  
ID ABU72461 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 904  
ID ABR99393 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 905  
ID ABR98783 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 906  
ID ABO16306 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 907  
ID ABR92206 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 908  
ID ABO18847 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 909  
ID ABR78268 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 910  
ID ABU85004 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 911  
ID ABO00143 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 912  
ID ABO11475 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 913  
ID ABO02120 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 914  
ID ABU88694 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 915  
ID ABU83389 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 916  
ID ABO06190 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 917  
ID ABR59226 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 918  
ID ABO09288 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 919  
ID ABO19152 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 920  
ID ABO11170 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 921  
ID ABR66788 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 922  
ID ABO16001 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 923  
ID ABO13707 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 924  
ID ABU65610 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, SEQ ID 84.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 925  
ID ABO07458 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 926  
ID ABO03645 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 927  
ID ABR67093 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027266-A1.

PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 928  
ID ABO15696 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 929  
ID ABU55977 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, PRO732.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 930  
ID ABU65305 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 931  
ID ABU95250 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 932  
ID ABU71153 standard; protein; 453 AA.  
DE Human PRO732 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 933  
ID ABO07763 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 934  
ID ABR70004 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 935  
ID ABR69337 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 936  
ID ABO01478 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 937  
ID ABU81280 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003017542-A1.

PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 938  
ID ABR60077 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 939  
ID ABR67812 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 940  
ID ABR65200 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 941  
ID ABR68422 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 942  
ID ABR71834 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 943  
ID ABU59210 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, #24.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 944  
ID ABU85314 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 945  
ID ABU89004 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 946  
ID ABU83084 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 947  
ID ABU94940 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 948
ID ABU90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 949
ID ABU83999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 950
ID ABU93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 951
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 952
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 953
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 954
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 955
ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 956
ID ABU56972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 957
ID ABU85924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;

Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 958
ID ABU82211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 959
ID ABU87222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 960
ID ABU83694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 961
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 962
ID ABU81779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 963
ID ABU65943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 964
ID ABR59772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 965
ID ABU93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 966
ID ABU99813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 967
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 968
ID ABR90901 standard; protein; 453 AA.
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Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 989  
ID ABR70919 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 990  
ID ABU87527 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 991  
ID ABU91395 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 992  
ID ABU84609 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 993  
ID ABR69699 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 994  
ID ABU80076 standard; protein; 453 AA.  
DE Human PRO protein #42.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 995  
ID ABU92125 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 996  
ID ABU93345 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 997  
ID ABO09898 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 998  
ID ABO08983 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 999  
ID ABU10831 standard; protein; 453 AA.

DE Human PRO polypeptide #17.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1000  
ID ABU10551 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein #42.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1001  
ID ABU81583 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1002  
ID ABU95560 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1003  
ID ABU96769 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1004  
ID ABR70614 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1005  
ID ABO04965 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1006  
ID ABO08373 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1007  
ID ABU88522 standard; protein; 453 AA.  
DE Human secreted and transmembrane polypeptide PRO732.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1008  
ID ABO34036 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1009
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1010
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1011
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1012
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1013
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1014
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1015
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1016
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1017
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1018
ID ABO31511 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1019
ID ABM07928 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1020
ID ABO40408 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1021
ID ABO35833 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1022
ID ABO43972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1023
ID ADA77836 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1024
ID ABM24767 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1025
ID ABO03035 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1026
ID ABR90291 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1027
ID ABM17205 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1028  
ID ABR94951 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1029  
ID ABR95256 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1030  
ID ABO21494 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1031  
ID ABR97758 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1032  
ID ABR87546 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1033  
ID ABM77587 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1034  
ID ABM27817 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1035  
ID ABM06098 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1036  
ID ABM03604 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1037  
ID ABO27546 standard; protein; 453 AA.

ID ABM35055 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1038  
ID ABM26292 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1039  
ID ABO48074 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1040  
ID ABR92816 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1041  
ID ABO24577 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1042  
ID ADA37584 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1043  
ID ABM11588 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1044  
ID ABM02689 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1045  
ID ABM15985 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;  
RESULT 1046  
ID ABO27546 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1047  
ID ABM29037 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1048  
ID ABM07013 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1049  
ID ABM21107 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1050  
ID ABM09453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1051  
ID ABO41323 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1052  
ID ABO36138 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1053  
ID ABO43667 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1054  
ID ABM76367 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1055  
ID ABM76063 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104548-A1.

PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1056  
ID ABM25682 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1057  
ID ABM25987 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1058  
ID ADA21270 standard; protein; 453 AA.  
DE Human secreted/transmembrane polypeptide PRO732.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1059  
ID ABO03340 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1060  
ID ABO02425 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1061  
ID ABR90596 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1062  
ID ABR73664 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1063  
ID ABO16916 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1064  
ID ABR94341 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1065  
ID ABR75848 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044929-A1.



PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1066  
ID ABR71224 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1067  
ID ABR93121 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1068  
ID ABR93426 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1069  
ID ADA10057 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, PRO732.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1070  
ID ABR87851 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1071  
ID ABO27851 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1072  
ID ABO29986 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1073  
ID ABO33195 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1074  
ID ABM04883 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;

Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1075  
ID ABM08843 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1076  
ID ABO36443 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1077  
ID ABO35528 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1078  
ID ABO39493 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1079  
ID ABM10368 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1080  
ID ABM11893 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1081  
ID ABO52039 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1082  
ID ABO52344 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1083  
ID ABO23662 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1084

ID ADA17601 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1085  
ID ABR97148 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1086  
ID ABR86936 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1087  
ID ABM10978 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1088  
ID ABM28122 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1089  
ID ABO32121 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1090  
ID ABM15248 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1091  
ID ABM06403 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1092  
ID ABM04214 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1093  
ID ABM22327 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1094  
ID ABM07623 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1095  
ID ABO40713 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1096  
ID ABM35360 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1097  
ID ABM33123 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1098  
ID ABO52649 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1099  
ID ABO50209 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1100  
ID ABU9203 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1101  
ID ABO04255 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1102  
ID ABO05885 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1103  
ID ABM18425 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1104  
ID ADA27709 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1105  
ID ABR97453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1106  
ID ABR80553 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1107  
ID ABM01164 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1108  
ID ABR88766 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1109  
ID ABM13418 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1110  
ID ABM20802 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1111  
ID ABO41933 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1112  
ID ABO42543 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1113  
ID ABM10063 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1114  
ID ABO38578 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1115  
ID ABM32818 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1116  
ID ABM22632 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1117  
ID ABM74843 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1118  
ID ADA79628 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1119  
ID ABR96233 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1120  
ID ABM02384 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1121  
ID ABR86326 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1122  
ID ABR86631 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1123  
ID ABM16595 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1124  
ID ABM29647 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1125  
ID ABO29071 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1126  
ID ABM23852 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1127  
ID ABM23242 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1128  
ID ABM22022 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1129  
ID ABO37663 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1130  
ID ABM28427 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1131  
ID ABM28732 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1132  
ID ABM66376 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1133  
ID ABM75758 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1134  
ID ABM34038 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1135  
ID ABM34343 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1136  
ID ABO20274 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1137  
ID ABO21189 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1138  
ID ABO22104 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1139  
ID ABR96538 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1140  
ID ADA94289 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1141  
ID ABR85716 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1142  
ID ABR99698 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1143  
ID ABM00554 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1144  
ID ABM00249 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1145  
ID ABO29681 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1146  
ID ABM23547 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1147  
ID ABM29342 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1148  
ID ABO38273 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1149  
ID ABO45573 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1150  
ID ABM20497 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1151  
ID ADA81355 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1152  
ID ABO16611 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1153  
ID ABO18237 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1154  
ID ABO22664 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1155  
ID ABO22969 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1156  
ID ABR92511 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1157  
ID ABR81468 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1158  
ID ABM77892 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1159  
ID ABR89681 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;



Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1160  
ID ABM26597 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1161  
ID ABM13723 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1162  
ID ABO28461 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1163  
ID ABO30291 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1164  
ID ABM07318 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1165  
ID ABM03909 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1166  
ID ABO37053 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1167  
ID ABO41628 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1168  
ID ABO35223 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1169

ID ABM25072 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1170  
ID ABO47464 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1171  
ID ABO47769 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1172  
ID ABO48379 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1173  
ID ABO51429 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1174  
ID ABO51734 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1175  
ID ABO50514 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1176  
ID ABR79638 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1177  
ID ABM16900 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1178  
ID ABO17932 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044918-A1.

PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1179  
ID ABO20884 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1180  
ID ABR96843 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1181  
ID ADA38514 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1182  
ID ABM12198 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1183  
ID ABM16290 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1184  
ID ABM24157 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1185  
ID ABM14638 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1186  
ID ABM04519 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1187  
ID ABM06708 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1188

ID ABM09148 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1189  
ID ABO39188 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1190  
ID ABM75453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1191  
ID ABM25377 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1192  
ID ABM19887 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1193  
ID ABO46793 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1194  
ID ABO47098 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1195  
ID ADA83153 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1196  
ID ABR71529 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1197  
ID ABR72139 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032136-A1.  
PD 13-FEB-2003.

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Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1198
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1199
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1200
ID ABR84801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1201
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1202
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1203
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1204
ID ABM18120 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1205
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1206
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1207
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.

Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1198
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1209
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1210
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1211
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1212
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1213
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1214
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1215
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1216
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
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RESULT 1217  
ID ABM05488 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1218  
ID ABM15553 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1219  
ID ABM08538 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1220  
ID ABO42238 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1221  
ID ABO37968 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1222  
ID ABO45878 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1223  
ID ABM66681 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1224  
ID ADB20196 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1225  
ID ABM19582 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1226  
ID ABO49294 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1227  
ID ABO49599 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1228  
ID ADA78448 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1229  
ID ABR88156 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1230  
ID ABM26902 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1231  
ID ABM03299 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1232  
ID ABO39798 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 6; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1233  
ID ABO49904 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1234  
ID ABO50819 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1235  
ID ABO05275 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1236  
ID ABR74579 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1237  
ID ABR77058 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1238  
ID ABM17815 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1239  
ID ABR95866 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1240  
ID ABO21799 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1241  
ID ABO19969 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1242  
ID ABO24272 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1243  
ID ABR86021 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1244  
ID ABM10673 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1245  
ID ABM76672 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1246  
ID ABR89376 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1247  
ID ABM12503 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1248  
ID ABM05793 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1249  
ID ABO34918 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1250  
ID ABM02994 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1251  
ID ABM18972 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1252  
ID ABM19277 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1253  
ID ABO46488 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1254  
ID ABO48989 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049757-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1255  
ID ABR69032 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1256  
ID ABR89071 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1257  
ID ABR72444 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1258  
ID ABR74274 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1259  
ID ABO18542 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1260  
ID ABR80248 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1261  
ID ABM01469 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1262  
ID ABM02079 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1263  
ID ABR87241 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1264

ID ABM12808 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1265  
ID ABM30562 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1266  
ID ABM24462 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1267  
ID ABO29376 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1268  
ID ABO31206 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1269  
ID ABM14333 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1270  
ID ABM09758 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1271  
ID ABO38883 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 6.1%; Score 84.5; DB 7; Length 453;  
Query Match 19.8%; Pred. No. 3.3;  
RESULT 1272  
ID ABM34648 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1273  
ID ABO51124 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.





PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1293  
ID ABM20192 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1294  
ID ABO48684 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1295  
ID ABO22492 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1296  
ID ABR72749 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1297  
ID ABO15391 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1298  
ID ABR85106 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1299  
ID ABO15086 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1300  
ID ABO17221 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1301  
ID ABM17510 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1302  
ID ADA06362 standard; protein; 453 AA.  
DE Human secreted/transmembrane PRO polypeptide #17.  
PN US2003049638-A1.

PD 13-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1303  
ID ADA39055 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1304  
ID ABR85411 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1305  
ID ABM76977 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1306  
ID ABO28156 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1307  
ID ABM22937 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1308  
ID ABM30257 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1309  
ID ABM21717 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1310  
ID ABM21412 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1311  
ID ABM14943 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;

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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1312
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1313
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1314
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1315
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1316
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1317
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1318
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1319
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1320
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1321
ID ABM31172 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1322
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1323
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1324
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1325
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1326
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1327
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1328
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1329
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1330
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
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Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1331
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1332
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1333
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1334
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1335
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1336
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1337
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1338
ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1339
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1340
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1341
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1342
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1343
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1344
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1345
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1346
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1347
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1348
ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1349
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 3.3;
RESULT 1350
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1351  
ID ADF95434 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1352  
ID ADG12249 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1353  
ID ADH08909 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1354  
ID ADI35254 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1355  
ID ADH99746 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1356  
ID ADL32690 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1357  
ID ADM30224 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 7; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1358  
ID ADE74221 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1359  
ID ADE74833 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1360  
ID ADF35199 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.

PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1361  
ID ADG11449 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1362  
ID ADF96046 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1363  
ID ADG04317 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1364  
ID ADG00477 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1365  
ID ADG82733 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1366  
ID ADH26014 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1367  
ID ADH19319 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1368  
ID ADH32983 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1369  
ID ADH20812 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;

Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1370  
ID ADH19852 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1371  
ID ADJS4722 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1372  
ID ADJ64493 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1373  
ID ADM31389 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1374  
ID ADM36436 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1375  
ID ADM40241 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1376  
ID ADN37849 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1377  
ID ADR09184 standard; protein; 453 AA.  
DE Human protein useful for treating neurological disease Seq 2690.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1378  
ID AEM80816 standard; protein; 453 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;

RESULT 1379  
ID ADR99176 standard; protein; 453 AA.  
DE KIAA1253, SEQ ID 182.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (FARB ) BAYER PHARM CORP.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1380  
ID ADV69528 standard; protein; 453 AA.  
DE Human tyrosine kinase 50 amino acid sequence - SEQ ID 2.  
PN CN1510134-A.  
PD 07-JUL-2004.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 6.1%; Score 84.5; DB 8; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1381  
ID AEA38376 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein cDNA, #86.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 6.1%; Score 84.5; DB 9; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1382  
ID AED50079 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2005163766-A1.  
PD 28-JUL-2005.  
Query Match 6.1%; Score 84.5; DB 9; Length 453;  
Best Local Similarity 19.8%; Pred. No. 3.3;  
RESULT 1383  
ID ADG10618 standard; protein; 472 AA.  
DE Human STAT6-activating protein, SEQ ID NO:208.  
PN WO200296943-A1.  
PD 05-DEC-2002.  
PA (ASAH ) ASahi Kasei Kogyo KK.  
Query Match 6.1%; Score 84.5; DB 7; Length 472;  
Best Local Similarity 19.8%; Pred. No. 3.5;  
RESULT 1384  
ID AAM41275 standard; protein; 477 AA.  
DE Human polypeptide SEQ ID NO 6206.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 84.5; DB 4; Length 477;  
Best Local Similarity 19.8%; Pred. No. 3.6;  
RESULT 1385  
ID AAG46716 standard; protein; 521 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 84.5; DB 3; Length 521;  
Best Local Similarity 19.0%; Pred. No. 4;  
RESULT 1386  
ID ABB93783 standard; protein; 562 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2994.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.1%; Score 84.5; DB 5; Length 562;  
Best Local Similarity 19.6%; Pred. No. 4.5;  
RESULT 1387  
ID AAG46715 standard; protein; 571 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 84.5; DB 3; Length 571;  
Best Local Similarity 19.0%; Pred. No. 4.5;  
RESULT 1388  
ID ADX95745 standard; protein; 600 AA.  
DE Plant full length insert polypeptide seqid 58409.  
PN US2004034888-A1.



PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 6.1%; Score 84.5; DB 8; Length 600;  
Best Local Similarity 23.0%; Pred. No. 4.9;  
RESULT 1389  
ID ADA36714 standard; protein; 241 AA.  
DE Acinetobacter baumannii protein #3875.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 6; Length 241;  
Best Local Similarity 22.8%; Pred. No. 1.6;  
RESULT 1390  
ID ABG61495 standard; protein; 318 AA.  
DE Iron uptake ABC transporter polypeptide #2.  
PN WO200234773-A2.  
PD 02-MAY-2002.  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
Query Match 6.0%; Score 84; DB 5; Length 318;  
Best Local Similarity 24.4%; Pred. No. 2.3;  
RESULT 1391  
ID ABU02362 standard; protein; 318 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1940.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.0%; Score 84; DB 6; Length 318;  
Best Local Similarity 24.4%; Pred. No. 2.3;  
RESULT 1392  
ID ADZ10513 standard; protein; 403 AA.  
DE P. gingivalis hypothetical protein SEQ ID 296.  
PN WO2005019249-A2.  
PD 03-MAR-2005.  
PA (UYFL) UNIV FLORIDA.  
Query Match 6.0%; Score 84; DB 9; Length 403;  
Best Local Similarity 21.9%; Pred. No. 3.2;  
RESULT 1393  
ID ABG10541 standard; protein; 480 AA.  
DE Novel human diagnostic protein #10532.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.0%; Score 84; DB 4; Length 480;  
Best Local Similarity 20.5%; Pred. No. 4.1;  
RESULT 1394  
ID ADL04919 standard; protein; 506 AA.  
DE M. catarrhalis protein #685.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 8; Length 506;  
Best Local Similarity 19.9%; Pred. No. 4.4;  
RESULT 1395  
ID ADS23392 standard; protein; 516 AA.  
DE Bacterial polypeptide #12425.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.0%; Score 84; DB 8; Length 516;  
Best Local Similarity 25.0%; Pred. No. 4.5;  
RESULT 1396  
ID ABO67632 standard; protein; 537 AA.  
DE Klebsiella pneumoniae polypeptide seqid 14149.

PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 7; Length 537;  
Best Local Similarity 18.7%; Pred. No. 4.8;  
RESULT 1397  
ID ABU38257 standard; protein; 575 AA.  
DE Protein encoded by Prokaryotic essential gene #23784.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 84; DB 6; Length 575;  
Best Local Similarity 20.3%; Pred. No. 5.2;  
RESULT 1398  
ID ABO73781 standard; protein; 602 AA.  
DE Pseudomonas aeruginosa polypeptide #5956.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 7; Length 602;  
Best Local Similarity 20.3%; Pred. No. 5.6;  
RESULT 1399  
ID ABO70835 standard; protein; 720 AA.  
DE Pseudomonas aeruginosa polypeptide #3010.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 7; Length 720;  
Best Local Similarity 21.8%; Pred. No. 7.1;  
RESULT 1400  
ID ABU32051 standard; protein; 1137 AA.  
DE Protein encoded by Prokaryotic essential gene #17578.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 84; DB 6; Length 1137;  
Best Local Similarity 18.6%; Pred. No. 13;  
RESULT 1401  
ID ABO67057 standard; protein; 1138 AA.  
DE Klebsiella pneumoniae polypeptide seqid 13574.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 84; DB 7; Length 1138;  
Best Local Similarity 18.6%; Pred. No. 13;  
RESULT 1402  
ID ADT60220 standard; protein; 294 AA.  
DE Plant polypeptide, SEQ ID 10297.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 6.0%; Score 83.5; DB 8; Length 294;  
Best Local Similarity 25.4%; Pred. No. 2.4;  
RESULT 1403  
ID ABU37874 standard; protein; 295 AA.  
DE Protein encoded by Prokaryotic essential gene #23401.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 83.5; DB 6; Length 295;  
Best Local Similarity 21.6%; Pred. No. 2.4;  
RESULT 1404  
ID AEF12231 standard; protein; 308 AA.  
DE Murine trace amine associated receptor 7b SEQ ID NO:50.  
PN US2006009441-A1.  
PD 12-JAN-2006.  
PA (EBEL/) EBELING M.  
PA (HOEN/) HOENER M.  
PA (LIND/) LINDEMANN L.  
Query Match 6.0%; Score 83.5; DB 10; Length 308;  
Best Local Similarity 28.6%; Pred. No. 2.5;  
RESULT 1405  
ID ADV88472 standard; protein; 333 AA.

DE Streptococcus agalactiae protein sequence, SEQ ID 866.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.0%; Score 83.5; DB 8; Length 333;  
Best Local Similarity 21.4%; Pred. No. 2.8;  
RESULT 1406  
ID ADV79725 standard; protein; 333 AA.  
DE Streptococcus agalactiae protein, SEQ ID 866.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.0%; Score 83.5; DB 8; Length 333;  
Best Local Similarity 21.4%; Pred. No. 2.8;  
RESULT 1407  
ID ADV81883 standard; protein; 333 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3024.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.0%; Score 83.5; DB 8; Length 333;  
Best Local Similarity 21.4%; Pred. No. 2.8;  
RESULT 1408  
ID AAR97984 standard; protein; 618 AA.  
DE DmORF1 potassium channel protein.  
PN WO9613520-A1.  
PD 09-MAY-1996.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Query Match 6.0%; Score 83.5; DB 2; Length 618;  
Best Local Similarity 19.9%; Pred. No. 6.6;  
RESULT 1409  
ID AAU07616 standard; protein; 618 AA.  
DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.  
PN WO200161006-A2.  
PD 23-AUG-2001.  
PA (BADI ) BASF CORP.  
Query Match 6.0%; Score 83.5; DB 4; Length 618;  
Best Local Similarity 19.9%; Pred. No. 6.6;  
RESULT 1410  
ID ABG30123 standard; protein; 1027 AA.  
DE Novel human diagnostic protein #30114.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.0%; Score 83.5; DB 4; Length 1027;  
Best Local Similarity 19.8%; Pred. No. 13;  
RESULT 1411  
ID ABU28293 standard; protein; 1090 AA.  
DE Protein encoded by Prokaryotic essential gene #13820.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 83.5; DB 6; Length 1090;  
Best Local Similarity 18.5%; Pred. No. 14;  
RESULT 1412  
ID AAG44538 standard; protein; 250 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 83; DB 3; Length 250;  
Best Local Similarity 21.7%; Pred. No. 2.2;  
RESULT 1413  
ID AAG66371 standard; protein; 305 AA.  
DE Human partial olfactory receptor-like protein OLF3 #2.  
PN WO200155179-A2.  
PD 02-AUG-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.0%; Score 83; DB 4; Length 305;  
Best Local Similarity 20.6%; Pred. No. 2.8;  
RESULT 1414

ID AAY85935 standard; protein; 318 AA.  
DE S. pneumoniae derived protein #144.  
PN WO9806734-A1.  
PD 19-FEB-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match 6.0%; Score 83; DB 2; Length 318;  
Best Local Similarity 24.4%; Pred. No. 3;  
RESULT 1415  
ID ADK46461 standard; protein; 318 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 2976.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 83; DB 8; Length 318;  
Best Local Similarity 24.4%; Pred. No. 3;  
RESULT 1416  
ID AAG71916 standard; protein; 319 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 6.0%; Score 83; DB 4; Length 319;  
Best Local Similarity 20.6%; Pred. No. 3;  
RESULT 1417  
ID AAB46999 standard; protein; 321 AA.  
DE Human OLFXY protein.  
PN DE19937839-A1.  
PD 15-FEB-2001.  
PA (BRUE/) BRUESS M.  
PA (BOEN/) BOENISCH H.  
Query Match 6.0%; Score 83; DB 4; Length 321;  
Best Local Similarity 20.6%; Pred. No. 3;  
RESULT 1418  
ID ABP95927 standard; protein; 321 AA.  
DE Human GPCR polypeptide SEQ ID NO 664.  
PN WO200216548-A2.  
PD 28-FEB-2002.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Query Match 6.0%; Score 83; DB 5; Length 321;  
Best Local Similarity 20.6%; Pred. No. 3;  
RESULT 1419  
ID ADU24127 standard; protein; 321 AA.  
DE Human aspartic peptidase enzyme #19.  
PN US2004219609-A1.  
PD 04-NOV-2004.  
PA (DAYA/) DAY A G.  
PA (ESTE/) ESTELL D A.  
PA (LYON/) LYONS E H.  
PA (YAOJ/) YAO J.  
Query Match 6.0%; Score 83; DB 8; Length 321;  
Best Local Similarity 20.6%; Pred. No. 3;  
RESULT 1420  
ID ADR96441 standard; protein; 336 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 5076.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 83; DB 8; Length 336;  
Best Local Similarity 24.4%; Pred. No. 3.2;  
RESULT 1421  
ID AEA60311 standard; protein; 336 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:5076.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.0%; Score 83; DB 9; Length 336;  
Best Local Similarity 24.4%; Pred. No. 3.2;  
RESULT 1422  
ID ABU43979 standard; protein; 355 AA.  
DE Protein encoded by Prokaryotic essential gene #29506.  
PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 83; DB 6; Length 355;  
Best Local Similarity 23.0%; Pred. No. 3.5;  
RESULT 1423  
ID ABO62213 standard; protein; 417 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8730.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 83; DB 7; Length 417;  
Best Local Similarity 20.8%; Pred. No. 4.4;  
RESULT 1424  
ID AAY66647 standard; protein; 455 AA.  
DE Membrane-bound protein PRO732.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH) GENENTECH INC.  
Query Match 6.0%; Score 83; DB 3; Length 455;  
Best Local Similarity 19.8%; Pred. No. 4.9;  
RESULT 1425  
ID AAB96670 standard; protein; 490 AA.  
DE Putative P. abyssi succinyl-CoA synthetase #5.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
PA (IFRE-) IFREMER INST FR RECH EXPL MER.  
Query Match 6.0%; Score 83; DB 4; Length 490;  
Best Local Similarity 23.6%; Pred. No. 5.5;  
RESULT 1426  
ID ABO70524 standard; protein; 542 AA.  
DE Pseudomonas aeruginosa polypeptide #2699.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 83; DB 7; Length 542;  
Best Local Similarity 20.2%; Pred. No. 6.3;  
RESULT 1427  
ID ADA33498 standard; protein; 632 AA.  
DE Acinetobacter baumannii protein #659.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.0%; Score 83; DB 6; Length 632;  
Best Local Similarity 25.1%; Pred. No. 7.7;  
RESULT 1428  
ID ABB65640 standard; protein; 774 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23712.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.0%; Score 83; DB 4; Length 774;  
Best Local Similarity 22.4%; Pred. No. 10;  
RESULT 1429  
ID AAU38963 standard; protein; 774 AA.  
DE Drosophila G-protein coupled receptor, GCPR #41.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.0%; Score 83; DB 4; Length 774;  
Best Local Similarity 22.4%; Pred. No. 10;  
RESULT 1430  
ID ADC35871 standard; protein; 774 AA.  
DE Drosophila G protein coupled receptor seq id 43.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 6.0%; Score 83; DB 7; Length 774;  
Best Local Similarity 22.4%; Pred. No. 10;  
RESULT 1431  
ID AAE38199 standard; protein; 802 AA.  
DE Fruit fly G protein-coupled receptor (GPCR) protein #48.  
PN WO2003052078-A2.

PD 26-JUN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.0%; Score 83; DB 7; Length 802;  
Best Local Similarity 22.4%; Pred. No. 11;  
RESULT 1432  
ID ABP70924 standard; protein; 2159 AA.  
DE Maize DEK1 from B73.  
PN WO2003011015-A2.  
PD 13-FEB-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 6.0%; Score 83; DB 6; Length 2159;  
Best Local Similarity 20.6%; Pred. No. 42;  
RESULT 1433  
ID ADT57399 standard; protein; 2159 AA.  
DE Plant polypeptide, SEQ ID 7476.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match 6.0%; Score 83; DB 8; Length 2159;  
Best Local Similarity 20.6%; Pred. No. 42;  
RESULT 1434  
ID ADS43623 standard; protein; 391 AA.  
DE Bacterial polypeptide #22053.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 82.5; DB 8; Length 391;  
Best Local Similarity 23.2%; Pred. No. 4.6;  
RESULT 1435  
ID ABU28011 standard; protein; 395 AA.  
DE Protein encoded by Prokaryotic essential gene #13538.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 82.5; DB 6; Length 395;  
Best Local Similarity 19.7%; Pred. No. 4.6;  
RESULT 1436  
ID AAW21009 standard; protein; 461 AA.  
DE H. pylori cell envelope transporter protein, hp5ell726orf7.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR) ASTRA AB.  
Query Match 5.9%; Score 82.5; DB 2; Length 461;  
Best Local Similarity 21.5%; Pred. No. 5.7;  
RESULT 1437  
ID ABO69393 standard; protein; 492 AA.  
DE Pseudomonas aeruginosa polypeptide #1568.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 82.5; DB 7; Length 492;  
Best Local Similarity 19.1%; Pred. No. 6.3;  
RESULT 1438  
ID ADN18812 standard; protein; 596 AA.  
DE Bacterial polypeptide #1465.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 82.5; DB 8; Length 596;  
Best Local Similarity 20.6%; Pred. No. 8.1;  
RESULT 1439  
ID ABG06558 standard; protein; 875 AA.  
DE Novel human diagnostic protein #6549.  
PN WO200175067-A2.  
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC. 5.9%; Score 82.5; DB 4; Length 875;  
Query Match  
Best Local Similarity 26.0%; Pred. No. 14;  
RESULT 1440  
ID ADJ69204 standard; protein; 1457 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1010.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES. 5.9%; Score 82.5; DB 7; Length 1457;  
Query Match  
Best Local Similarity 26.0%; Pred. No. 28;  
RESULT 1441  
ID ADJ69205 standard; protein; 1457 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1011.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES. 5.9%; Score 82.5; DB 7; Length 1457;  
Query Match  
Best Local Similarity 26.0%; Pred. No. 28;  
RESULT 1442  
ID ADJ58460 standard; protein; 1457 AA.  
DE BAB13458.1(P450G5) protein.  
PN WO2004011648-A2.  
PD 05-FEB-2004.  
PA (INPH-) INPHARMATICA LTD. 5.9%; Score 82.5; DB 8; Length 1457;  
Query Match  
Best Local Similarity 26.0%; Pred. No. 28;  
RESULT 1443  
ID ADC31246 standard; protein; 2548 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1328.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC. 5.9%; Score 82.5; DB 7; Length 2548;  
Query Match  
Best Local Similarity 26.0%; Pred. No. 60;  
RESULT 1444  
ID ABO84919 standard; protein; 219 AA.  
DE Human cancer-associated protein (CAP) HP07-069.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC. 5.9%; Score 82; DB 8; Length 219;  
Query Match  
Best Local Similarity 22.1%; Pred. No. 2.3;  
RESULT 1445  
ID AAB87783 standard; protein; 299 AA.  
DE Rat T2R03 amino acid sequence SEQ ID NO:81.  
PN WO200118050-A2.  
PD 15-MAR-2001.  
PA (REGC ) UNIV CALIFORNIA.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES. 5.9%; Score 82; DB 4; Length 299;  
Query Match  
Best Local Similarity 22.8%; Pred. No. 3.6;  
RESULT 1446  
ID ADJ84452 standard; protein; 299 AA.  
DE Rat T2R G-protein coupled receptor seq id 5.  
PN US2004038312-A1.  
PD 26-FEB-2004.  
PA (ZUKE/) ZUKER C S.  
PA (ADLE/) ADLER J E.  
PA (HOON/) HOON M.  
PA (RYBA/) RYBA N.  
PA (MUEL/) MUELLER K. 5.9%; Score 82; DB 8; Length 299;  
Query Match  
Best Local Similarity 22.8%; Pred. No. 3.6;  
RESULT 1447  
ID ADR29142 standard; protein; 299 AA.  
DE Taste receptor modulation-related rat T2R03 protein sequence SeqID81.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC. 5.9%; Score 82; DB 8; Length 299;  
Query Match

Best Local Similarity 22.8%; Pred. No. 3.6;  
RESULT 1448  
ID AAB10684 standard; protein; 356 AA.  
DE A. thaliana PUP1 protein.  
PN DE19907209-A1.  
PD 24-AUG-2000.  
PA (FROM/) FROMMER W. 5.9%; Score 82; DB 3; Length 356;  
Query Match  
Best Local Similarity 19.4%; Pred. No. 4.6;  
RESULT 1449  
ID ABB91157 standard; protein; 356 AA.  
DE Herbicidally active polypeptide SEQ ID NO 368.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG. 5.9%; Score 82; DB 5; Length 356;  
Query Match  
Best Local Similarity 19.4%; Pred. No. 4.6;  
RESULT 1450  
ID ABU28157 standard; protein; 417 AA.  
DE Protein encoded by Prokaryotic essential gene #13684.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. 5.9%; Score 82; DB 6; Length 417;  
Query Match  
Best Local Similarity 27.1%; Pred. No. 5.7;  
RESULT 1451  
ID ADX68336 standard; protein; 440 AA.  
DE Plant full length insert polypeptide seqid 39179.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y. 5.9%; Score 82; DB 8; Length 440;  
Query Match  
Best Local Similarity 24.4%; Pred. No. 6.1;  
RESULT 1452  
ID ADK16901 standard; protein; 465 AA.  
DE Nanoarchaeum equitans cancer-associated (CA) protein #426.  
PN WO2003093434-A2.  
PD 13-NOV-2003.  
PA (DIVE-) DIVERSA CORP. 5.9%; Score 82; DB 8; Length 465;  
Query Match  
Best Local Similarity 23.7%; Pred. No. 6.6;  
RESULT 1453  
ID ABO81608 standard; protein; 474 AA.  
DE Pseudomonas aeruginosa polypeptide #13783.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP. 5.9%; Score 82; DB 7; Length 474;  
Query Match  
Best Local Similarity 20.1%; Pred. No. 6.8;  
RESULT 1454  
ID ADY13455 standard; protein; 478 AA.  
DE Plant full length insert polypeptide seqid 69270.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y. 5.9%; Score 82; DB 8; Length 478;  
Query Match  
Best Local Similarity 23.3%; Pred. No. 6.8;  
RESULT 1455  
ID ADN23219 standard; protein; 573 AA.  
DE Bacterial polypeptide #5872.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 82; DB 8; Length 573;  
Best Local Similarity 18.5%; Pred. No. 8.8;  
RESULT 1456  
ID ADN23218 standard; protein; 573 AA.  
DE Bacterial polypeptide #5871.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 82; DB 8; Length 573;  
Best Local Similarity 18.5%; Pred. No. 8.8;  
RESULT 1457  
ID ABU50193 standard; protein; 1139 AA.  
DE Protein encoded by Prokaryotic essential gene #35720.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 82; DB 6; Length 1139;  
Best Local Similarity 19.5%; Pred. No. 23;  
RESULT 1458  
ID AAE04312 standard; protein; 1167 AA.  
DE Human modified cardiac adenylcyclase VI (ACVI) isoform.  
PN WO200148164-A2.  
PD 05-JUL-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 5.9%; Score 82; DB 4; Length 1167;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1459  
ID ABG32870 standard; protein; 1167 AA.  
DE Chimaeric Adenylcyclase isoform 6, AC-VI.  
PN US2002103147-A1.  
PD 01-AUG-2002.  
PA (HAMM/) HAMMOND H K.  
PA (INSE/) INSEL P A.  
PA (PING/) PING P.  
PA (POST/) POST S R.  
PA (GAOM/) GAO M.  
Query Match 5.9%; Score 82; DB 5; Length 1167;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1460  
ID AAW30599 standard; protein; 1168 AA.  
DE Human type VI adenyl cyclase.  
PN WO9901547-A1.  
PD 14-JAN-1999.  
PA (CORT-) COR THERAPEUTICS INC.  
Query Match 5.9%; Score 82; DB 2; Length 1168;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1461  
ID AAE04311 standard; protein; 1168 AA.  
DE Human cardiac adenylcyclase VI (ACVI) isoform #2.  
PN WO200148164-A2.  
PD 05-JUL-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 5.9%; Score 82; DB 4; Length 1168;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1462  
ID ABG32869 standard; protein; 1168 AA.  
DE Human Adenylcyclase isoform 6, AC-VI, #2.  
PN US2002103147-A1.  
PD 01-AUG-2002.  
PA (HAMM/) HAMMOND H K.  
PA (INSE/) INSEL P A.  
PA (PING/) PING P.  
PA (POST/) POST S R.  
PA (GAOM/) GAO M.  
Query Match 5.9%; Score 82; DB 5; Length 1168;

Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1463  
ID ADE56876 standard; protein; 1168 AA.  
DE Human Protein O43306, SEQ ID NO 2731.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.9%; Score 82; DB 7; Length 1168;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1464  
ID ADQ89850 standard; protein; 1168 AA.  
DE Antagonist of cell cycle progression polypeptide #140.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 5.9%; Score 82; DB 8; Length 1168;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1465  
ID ADX98516 standard; protein; 1168 AA.  
DE Human adenylate cyclase 6 (ADCY6) protein.  
PN WO2005017121-A2.  
PD 24-FEB-2005.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.9%; Score 82; DB 9; Length 1168;  
Best Local Similarity 20.2%; Pred. No. 23;  
RESULT 1466  
ID ADK46612 standard; protein; 199 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3127.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 81.5; DB 8; Length 199;  
Best Local Similarity 20.2%; Pred. No. 2.3;  
RESULT 1467  
ID ABU02196 standard; protein; 205 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1774.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 5.9%; Score 81.5; DB 6; Length 205;  
Best Local Similarity 20.2%; Pred. No. 2.4;  
RESULT 1468  
ID AAY81546 standard; protein; 206 AA.  
DE Streptococcus pneumoniae type 4 protein sequence #46.  
PN WO200006737-A2.  
PD 10-FEB-2000.  
PA (MICR-) MICROBIAL TECHNIQS LTD.  
Query Match 5.9%; Score 81.5; DB 3; Length 206;  
Best Local Similarity 20.2%; Pred. No. 2.5;  
RESULT 1469  
ID ADR96056 standard; protein; 208 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4691.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 81.5; DB 8; Length 208;  
Best Local Similarity 20.2%; Pred. No. 2.5;  
RESULT 1470  
ID AEA59926 standard; protein; 208 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4691.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 5.9%; Score 81.5; DB 9; Length 208;  
Best Local Similarity 20.2%; Pred. No. 2.5;  
RESULT 1471  
ID ABU41035 standard; protein; 278 AA.  
DE Protein encoded by Prokaryotic essential gene #26562.  
PN WO200277183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 81.5; DB 6; Length 278;  
Best Local Similarity 21.0%; Pred. No. 3.7;  
RESULT 1472  
ID ADF05890 standard; protein; 280 AA.  
DE Bacterial polypeptide #2003.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 81.5; DB 7; Length 280;  
Best Local Similarity 21.0%; Pred. No. 3.7;  
RESULT 1473  
ID ADY10132 standard; protein; 332 AA.  
DE Plant full length insert polypeptide seqid 65947.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.9%; Score 81.5; DB 8; Length 332;  
Best Local Similarity 21.8%; Pred. No. 4.7;  
RESULT 1474  
ID ABB91156 standard; protein; 351 AA.  
DE Herbicidally active polypeptide SEQ ID NO 367.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 5.9%; Score 81.5; DB 5; Length 351;  
Best Local Similarity 23.1%; Pred. No. 5.1;  
RESULT 1475  
ID AAM93355 standard; protein; 399 AA.  
DE Human polypeptide, SEQ ID NO: 2909.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.9%; Score 81.5; DB 4; Length 399;  
Best Local Similarity 22.6%; Pred. No. 6.1;  
RESULT 1476  
ID ADL30876 standard; protein; 399 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 2909.  
PN EP1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.9%; Score 81.5; DB 8; Length 399;  
Best Local Similarity 22.6%; Pred. No. 6.1;  
RESULT 1477  
ID ABU39717 standard; protein; 425 AA.  
DE Protein encoded by Prokaryotic essential gene #25244.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 81.5; DB 6; Length 425;  
Best Local Similarity 19.6%; Pred. No. 6.6;  
RESULT 1478  
ID AAU33707 standard; protein; 438 AA.  
DE Pseudomonas aeruginosa cellular proliferation protein #151.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 81.5; DB 4; Length 438;  
Best Local Similarity 20.3%; Pred. No. 6.9;  
RESULT 1479  
ID ABU15597 standard; protein; 438 AA.  
DE Protein encoded by Prokaryotic essential gene #1124.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 81.5; DB 6; Length 438;  
Best Local Similarity 20.3%; Pred. No. 6.9;  
RESULT 1480

ID ABO83917 standard; protein; 503 AA.  
DE Pseudomonas aeruginosa polypeptide #16092.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 81.5; DB 7; Length 503;  
Best Local Similarity 20.3%; Pred. No. 8.4;  
RESULT 1481  
ID ABP65039 standard; protein; 234 AA.  
DE Mouse membrane spanning 4-domain family, subfamily A 7 protein.  
PN WO200262946-A2.  
PD 15-AUG-2002.  
PA (UYDU-) UNIV DUKE.  
Query Match 5.8%; Score 81; DB 5; Length 234;  
Best Local Similarity 20.6%; Pred. No. 3.3;  
RESULT 1482  
ID ADD43824 standard; protein; 293 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 119.  
PN WO2003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.8%; Score 81; DB 7; Length 293;  
Best Local Similarity 18.4%; Pred. No. 4.5;  
RESULT 1483  
ID AEA19116 standard; protein; 293 AA.  
DE Chlamydia trachomatis protein - SEQ ID 119.  
PN US2005106162-A1.  
PD 19-MAY-2005.  
PA (GRAN/) GRANDI G.  
PA (RATT/) RATTI G.  
Query Match 5.8%; Score 81; DB 9; Length 293;  
Best Local Similarity 18.4%; Pred. No. 4.5;  
RESULT 1484  
ID ADA34894 standard; protein; 323 AA.  
DE Acinetobacter baumannii protein #2055.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 81; DB 6; Length 323;  
Best Local Similarity 22.5%; Pred. No. 5.2;  
RESULT 1485  
ID AAO20532 standard; protein; 392 AA.  
DE Protein of the human TFM-2 gene sequence.  
PN WO200229041-A2.  
PD 11-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.8%; Score 81; DB 5; Length 392;  
Best Local Similarity 17.8%; Pred. No. 6.8;  
RESULT 1486  
ID AEF18943 standard; protein; 392 AA.  
DE Human Transporter Family Member-2, TFM-2.  
PN US2006008819-A1.  
PD 12-JAN-2006.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.8%; Score 81; DB 10; Length 392;  
Best Local Similarity 17.8%; Pred. No. 6.8;  
RESULT 1487  
ID ADD37455 standard; protein; 394 AA.  
DE Human transporter TFM-2.  
PN US2003143675-A1.  
PD 31-JUL-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.8%; Score 81; DB 7; Length 394;  
Best Local Similarity 17.8%; Pred. No. 6.8;  
RESULT 1488  
ID ABO61692 standard; protein; 425 AA.  
DE Klebsiella pneumoniae polypeptide seqid 8209.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 81; DB 7; Length 425;  
Best Local Similarity 22.7%; Pred. No. 7.6;  
RESULT 1489



ID AAE21184 standard; protein; 515 AA.  
DE Human TRICH-28 protein.  
PN WO200212340-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.8%; Score 81; DB 5; Length 515;  
Best Local Similarity 17.8%; Pred. No. 9.9;  
RESULT 1490  
ID ABJ37907 standard; protein; 515 AA.  
DE NOVX protein sequence SEQ ID NO 60.  
PN WO200281517-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.8%; Score 81; DB 6; Length 515;  
Best Local Similarity 17.8%; Pred. No. 9.9;  
RESULT 1491  
ID ADQ66916 standard; protein; 515 AA.  
DE Novel human protein sequence #1889.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.8%; Score 81; DB 8; Length 515;  
Best Local Similarity 17.8%; Pred. No. 9.9;  
RESULT 1492  
ID ABO84581 standard; protein; 515 AA.  
DE Human cancer-associated protein HP17-001.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.8%; Score 81; DB 8; Length 515;  
Best Local Similarity 17.8%; Pred. No. 9.9;  
RESULT 1493  
ID ADH58563 standard; protein; 516 AA.  
DE Human Na+-independent transporter-related transporter protein.  
PN WO2003076644-A2.  
PD 18-SEP-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 5.8%; Score 81; DB 7; Length 516;  
Best Local Similarity 17.8%; Pred. No. 9.9;  
RESULT 1494  
ID ADN23220 standard; protein; 544 AA.  
DE Bacterial polypeptide #5873.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.8%; Score 81; DB 8; Length 544;  
Best Local Similarity 23.0%; Pred. No. 11;  
RESULT 1495  
ID ABB64860 standard; protein; 875 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21372.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 5.8%; Score 81; DB 4; Length 875;  
Best Local Similarity 20.9%; Pred. No. 20;  
RESULT 1496  
ID ABU39716 standard; protein; 1102 AA.  
DE Protein encoded by Prokaryotic essential gene #25243.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 81; DB 6; Length 1102;  
Best Local Similarity 20.0%; Pred. No. 28;  
RESULT 1497  
ID ADY52908 standard; protein; 260 AA.  
DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 4.  
PN WO2005019461-A2.  
PD 03-MAR-2005.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.

Query Match 5.8%; Score 80.5; DB 9; Length 260;  
Best Local Similarity 21.1%; Pred. No. 4.4;  
RESULT 1498  
ID ADY52974 standard; protein; 264 AA.  
DE Nodularia spumigena ketocarotenoid-related ketolase protein - SEQ ID 70.  
PN WO2005019461-A2.  
PD 03-MAR-2005.  
PA (SUNG-) SUNGENE GMBH & CO KGAA.  
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Best Local Similarity 21.1%; Pred. No. 4.5;  
RESULT 1499  
ID ABO65403 standard; protein; 298 AA.  
DE Klebsiella pneumoniae polypeptide seqid 11920.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 80.5; DB 7; Length 298;  
Best Local Similarity 18.5%; Pred. No. 5.3;  
RESULT 1500  
ID ABB32477 standard; protein; 359 AA.  
DE Staphylococcus aureus polypeptide SEQ ID NO 14.  
PN WO200177365-A2.  
PD 18-OCT-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 5.8%; Score 80.5; DB 5; Length 359;  
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OM protein - protein search, using sw model

Run on: August 28, 2006, 17:41:45 ; Search time 50 Seconds  
(without alignments)  
465.663 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

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Post-processing: Minimum Match 0%  
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES			
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1	1392	100.0	Sequence 23, Appl
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11	1392	100.0	Sequence 23, Appl
12	1388	99.7	Sequence 190, App
13	595.5	42.8	Sequence 96, Appl
14	479.5	34.4	Sequence 38, Appl
15	358	25.7	Sequence 130, App
16	358	25.7	Sequence 224, App
17	118	8.5	Sequence 20, Appl
18	118	8.5	Sequence 20, Appl
19	118	8.5	Sequence 20, Appl
20	118	8.5	Sequence 2, Appli
21	118	8.5	Sequence 2, Appli
22	118	8.5	Sequence 2, Appli
23	118	8.5	Sequence 20, Appl
24	91.5	6.6	Sequence 4147, Ap
25	91.5	6.6	Sequence 14, Appl
26	90	6.5	Sequence 588, App

27	90	6.5	2	US-09-248-796A-20434	Sequence 20434, A
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29	88	6.3	2	US-09-248-796A-16383	Sequence 16383, A
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31	86.5	6.2	2	US-09-134-000C-4914	Sequence 4914, Ap
32	85.5	6.1	2	US-09-786-681A-4	Sequence 4, Appli
33	85.5	6.1	2	US-09-786-681A-2	Sequence 2, Appli
34	85	6.1	2	US-09-948-774-2	Sequence 2, Appli
35	85	6.1	2	US-08-726-214-12	Sequence 12, Appl
36	84.5	6.1	2	US-09-134-000C-6205	Sequence 6205, Ap
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42	84.5	6.1	2	US-09-989-735-73	Sequence 73, Appl
43	84.5	6.1	3	US-09-989-726-73	Sequence 73, Appl
44	84.5	6.1	3	US-09-997-514-73	Sequence 73, Appl
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63	82	5.9	3	US-10-770-127-81	Sequence 81, Appl
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65	82	5.9	2	US-09-248-796A-20154	Sequence 20154, A
66	82	5.9	2	US-09-248-796A-17191	Sequence 17191, A
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70	82	5.9	2	US-09-949-016-8862	Sequence 8862, Ap
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72	82	5.9	2	US-09-472-667-11	Sequence 11, Appl
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104	79.5	5.7	831	1	US-08-677-734A-11	Sequence 11, Appl	177	74.5	5.4	436	7	5432081-10	Patent No. 5432081
105	79.5	5.7	831	2	US-09-097-053-11	Sequence 11, Appl	178	74.5	5.4	443	2	US-09-328-352-7069	Sequence 7069, Ap
106	79	5.7	298	2	US-09-438-185A-545	Sequence 545, App	179	74.5	5.4	475	2	US-09-248-796A-20067	Sequence 20067, A
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110	79	5.7	670	2	US-09-489-039A-7251	Sequence 7251, Ap	183	74.5	5.4	832	2	US-09-605-703B-356	Sequence 356, App
111	78.5	5.6	320	4	US-10-038-895A-5	Sequence 5, Appli	184	74.5	5.4	1798	2	US-09-270-767-44775	Sequence 44775, A
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113	78.5	5.6	793	2	US-09-900-237-18	Sequence 18, Appl	186	74	5.3	173	2	US-09-328-352-6026	Sequence 6026, Ap
114	78.5	5.6	832	1	US-08-677-734A-12	Sequence 12, Appl	187	74	5.3	262	2	US-09-328-352-6026	Sequence 6026, Ap
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116	78	5.6	221	2	US-09-248-796A-16814	Sequence 16814, A	189	74	5.3	280	2	US-09-438-185A-829	Sequence 829, App
117	78	5.6	292	2	US-09-540-236-3287	Sequence 3287, Ap	190	74	5.3	282	2	US-09-583-110-3219	Sequence 3219, Ap
118	78	5.6	405	2	US-09-144-914-5	Sequence 5, Appli	191	74	5.3	292	1	US-09-024-848-2	Sequence 2, Appli
119	78	5.6	575	2	US-09-328-352-6465	Sequence 6465, Ap	192	74	5.3	292	2	US-09-348-116A-2	Sequence 2, Appli
120	78	5.6	664	2	US-09-902-540-16458	Sequence 16458, A	193	74	5.3	307	2	US-09-303-518D-408	Sequence 408, App
121	77.5	5.6	238	2	US-09-328-352-7122	Sequence 7122, Ap	194	74	5.3	332	2	US-09-902-540-15291	Sequence 15291, A
122	77.5	5.6	287	2	US-09-543-681A-5282	Sequence 5282, Ap	195	74	5.3	407	2	US-09-303-518D-802	Sequence 802, App
123	77.5	5.6	525	2	US-09-252-991A-27543	Sequence 27543, A	196	74	5.3	445	2	US-08-937-834-5	Sequence 5, Appli
124	77.5	5.6	693	2	US-10-094-749-2517	Sequence 2517, Ap	197	74	5.3	448	2	US-09-543-681A-7245	Sequence 7245, Ap
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127	77	5.5	318	2	US-09-710-279-3118	Sequence 3118, Ap	200	74	5.3	800	2	US-09-134-001C-5655	Sequence 5655, Ap
128	77	5.5	385	2	US-09-540-236-3736	Sequence 3736, Ap	201	74	5.3	937	2	US-09-949-002-536	Sequence 536, App
129	77	5.5	506	2	US-09-719-919A-1	Sequence 1, Appli	202	73.5	5.3	297	2	US-09-489-039A-8466	Sequence 8466, Ap
130	77	5.5	532	2	US-09-107-532A-7299	Sequence 7299, Ap	203	73.5	5.3	360	1	US-08-597-236-11	Sequence 11, Appl
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139	76	5.5	361	2	US-09-482-273-236	Sequence 236, App	212	73.5	5.3	416	2	US-09-543-681A-5455	Sequence 5455, Ap
140	76	5.5	378	2	US-09-107-532A-6500	Sequence 6500, Ap	213	73.5	5.3	417	2	US-09-107-532A-4001	Sequence 4001, Ap
141	76	5.5	424	2	US-09-252-991A-18895	Sequence 18895, A	214	73.5	5.3	428	2	US-09-198-452A-720	Sequence 720, App
142	76	5.5	429	2	US-09-922-501-10	Sequence 10, Appl	215	73.5	5.3	428	2	US-09-438-185A-682	Sequence 682, App
143	76	5.5	435	7	5268463-9	Patent No. 5268463	216	73.5	5.3	514	2	US-09-489-039A-11902	Sequence 11902, A
144	76	5.5	453	2	US-09-252-991A-17394	Sequence 17394, A	217	73.5	5.3	564	2	US-09-902-540-16018	Sequence 16018, A
145	76	5.5	633	2	US-09-949-016-10337	Sequence 10337, A	218	73.5	5.3	607	1	US-07-959-943-7	Sequence 7, Appli
146	75.5	5.4	313	2	US-09-252-991A-27163	Sequence 27163, A	219	73.5	5.3	630	1	US-07-959-943-9	Sequence 9, Appli
147	75.5	5.4	401	2	US-09-489-039A-11546	Sequence 11546, A	220	73.5	5.3	693	2	US-09-252-991A-19167	Sequence 19167, A
148	75.5	5.4	445	2	US-09-328-352-6669	Sequence 6669, Ap	221	73.5	5.3	717	2	US-09-134-000C-5833	Sequence 5833, Ap
149	75.5	5.4	517	2	US-09-248-796A-20437	Sequence 20437, A	222	73.5	5.3	1099	2	US-08-726-214-14	Sequence 14, Appl
150	75.5	5.4	717	2	US-09-854-122-49	Sequence 49, Appl	223	73.5	5.3	2020	1	US-07-551-531-2	Sequence 2, Appli
151	75.5	5.4	1155	2	US-09-543-681A-6286	Sequence 6286, Ap	224	73.5	5.3	2485	5	PCT-US94-00198-1	Sequence 1, Appli
152	75.5	5.4	1172	2	US-09-328-352-6071	Sequence 6071, Ap	225	73.5	5.3	2485	5	PCT-US94-00198-2	Sequence 1, Appli
153	75	5.4	218	2	US-09-328-352-5215	Sequence 5215, Ap	226	73.5	5.3	2818	1	US-08-510-284-1	Sequence 1, Appli
154	75	5.4	283	2	US-09-107-433-3024	Sequence 3024, Ap	227	73.5	5.3	2818	1	US-08-411-389-2	Sequence 2, Appli
155	75	5.4	290	2	US-09-134-001C-4893	Sequence 4893, Ap	228	73.5	5.3	2818	1	US-08-449-933-2	Sequence 2, Appli
156	75	5.4	344	1	US-08-689-974-1	Sequence 1, Appli	229	73.5	5.3	2818	2	US-07-966-049A-2	Sequence 2, Appli
157	75	5.4	344	2	US-09-058-376-1	Sequence 4, Appli	230	73.5	5.3	2818	2	US-09-542-331-2	Sequence 2, Appli
158	75	5.4	394	2	US-09-144-914-4	Sequence 4, Appli	231	73.5	5.3	2818	2	US-09-510-791-2	Sequence 2, Appli
159	75	5.4	394	2	US-09-655-272-5	Sequence 5, Appli	232	73	5.2	178	2	US-09-328-352-5593	Sequence 5593, Ap
160	75	5.4	399	2	US-09-489-039A-9414	Sequence 9414, Ap	233	73	5.2	187	2	US-09-328-352-7918	Sequence 7918, Ap
161	75	5.4	408	2	US-09-719-088B-2	Sequence 2, Appli	234	73	5.2	234	2	US-09-270-767-45527	Sequence 45527, A
162	75	5.4	420	2	US-09-255-368-6	Sequence 6, Appli	235	73	5.2	291	2	US-09-252-991A-32938	Sequence 32938, A
163	75	5.4	420	2	US-09-405-558-6	Sequence 6, Appli	236	73	5.2	431	2	US-09-710-279-2566	Sequence 2566, Ap
164	75	5.4	420	2	US-09-538-036-6	Sequence 6, Appli	237	73	5.2	434	2	US-09-328-352-7304	Sequence 7304, Ap
165	75	5.4	457	2	US-09-489-039A-8037	Sequence 8037, Ap	238	73	5.2	445	1	US-08-900-148-2	Sequence 2, Appli
166	75	5.4	524	2	US-09-248-796A-20256	Sequence 20256, A	239	73	5.2	466	2	US-09-134-001C-3355	Sequence 3355, Ap
167	75	5.4	579	2	US-09-720-317A-4	Sequence 4, Appli	240	73	5.2	727	2	US-09-815-923-10	Sequence 10, Appl
168	74.5	5.4	304	2	US-09-328-352-6459	Sequence 6459, Ap	241	73	5.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
169	74.5	5.4	321	2	US-09-252-991A-31084	Sequence 31084, A	242	72.5	5.2	287	2	US-09-583-110-3621	Sequence 3621, Ap
170	74.5	5.4	340	2	US-09-543-681A-5778	Sequence 5778, Ap	243	72.5	5.2	281	2	US-09-540-236-2349	Sequence 2349, Ap
171	74.5	5.4	367	2	US-09-198-452A-1069	Sequence 1069, Ap	244	72.5	5.2	319	2	US-09-543-681A-5398	Sequence 5398, Ap
172	74.5	5.4	367	2	US-09-438-185A-996	Sequence 996, App	245	72.5	5.2	389	2	US-09-328-352-5055	Sequence 5055, Ap

246	72.5	5.2	413	2	US-09-540-236-3672	Sequence 3672, Ap	319	71	5.1	384	2	US-09-902-540-11956	Sequence 11956, A
247	72.5	5.2	519	2	US-09-489-039A-13346	Sequence 13346, A	320	71	5.1	388	2	US-09-222-938A-37	Sequence 37, Appl
248	72.5	5.2	519	2	US-09-248-796A-20368	Sequence 20368, A	321	71	5.1	397	2	US-09-583-110-2946	Sequence 2946, Ap
249	72.5	5.2	607	2	US-09-328-352-5096	Sequence 5096, Ap	322	71	5.1	404	2	US-09-107-433-3747	Sequence 3747, Ap
250	72	5.2	261	2	US-09-538-092-318	Sequence 318, App	323	71	5.1	408	2	US-09-489-039A-9583	Sequence 9583, Ap
251	72	5.2	273	2	US-09-328-352-5843	Sequence 5843, Ap	324	71	5.1	454	2	US-09-489-847-305	Sequence 305, Appl
252	72	5.2	337	2	US-09-902-540-13005	Sequence 13005, A	325	71	5.1	461	2	US-09-043-944-1	Sequence 1, Appli
253	72	5.2	347	2	US-09-303-518D-804	Sequence 804, App	326	71	5.1	461	2	US-09-043-944-6	Sequence 6, Appli
254	72	5.2	355	2	US-09-170-496D-2	Sequence 2, Appli	327	71	5.1	461	2	US-10-811-199-1	Sequence 1, Appli
255	72	5.2	430	2	US-09-134-001C-2981	Sequence 2981, Ap	328	71	5.1	461	2	US-10-811-199-6	Sequence 6, Appli
256	72	5.2	468	2	US-09-543-681A-4671	Sequence 4671, Ap	329	71	5.1	465	2	US-09-710-279-1676	Sequence 1676, Ap
257	72	5.2	495	2	US-09-359-167-4	Sequence 4, Appli	330	71	5.1	466	2	US-09-328-352-7117	Sequence 7117, Ap
258	72	5.2	502	2	US-09-579-250-12	Sequence 12, Appl	331	71	5.1	502	1	US-08-278-635B-7	Sequence 7, Appli
259	72	5.2	502	2	US-09-579-250-14	Sequence 14, Appl	332	71	5.1	502	1	US-08-466-589-8	Sequence 8, Appli
260	72	5.2	506	2	US-09-252-991A-25852	Sequence 25852, A	333	71	5.1	502	1	US-08-700-636-8	Sequence 8, Appli
261	72	5.2	569	1	US-08-750-723A-2	Sequence 2, Appli	334	71	5.1	502	1	US-08-464-258B-7	Sequence 7, Appli
262	72	5.2	569	2	US-09-191-275-2	Sequence 2, Appli	335	71	5.1	502	2	US-08-467-574-8	Sequence 8, Appli
263	72	5.2	906	1	US-08-190-802A-31	Sequence 31, Appl	336	71	5.1	502	2	US-08-471-961-7	Sequence 7, Appli
264	72	5.2	906	2	US-08-477-346-31	Sequence 31, Appl	337	71	5.1	502	2	US-09-217-345-8	Sequence 8, Appli
265	72	5.2	906	2	US-08-473-089-31	Sequence 31, Appl	338	71	5.1	502	2	US-08-487-596-12	Sequence 12, Appl
266	72	5.2	906	2	US-08-487-072A-31	Sequence 31, Appl	339	71	5.1	502	2	US-09-345-109C-7	Sequence 7, Appli
267	71.5	5.1	228	2	US-09-973-278-160	Sequence 160, App	340	71	5.1	502	2	US-09-892-985-8	Sequence 8, Appli
268	71.5	5.1	229	2	US-09-227-357-237	Sequence 237, App	341	71	5.1	502	2	US-09-579-250-2	Sequence 2, Appli
269	71.5	5.1	237	1	US-08-818-514-3	Sequence 3, Appli	342	71	5.1	502	2	US-09-579-250-10	Sequence 10, Appl
270	71.5	5.1	237	2	US-09-115-934A-3	Sequence 3, Appli	343	71	5.1	502	2	US-09-703-951A-12	Sequence 12, Appl
271	71.5	5.1	237	2	US-09-611-175-3	Sequence 3, Appli	344	71	5.1	571	2	US-09-252-991A-28549	Sequence 28549, A
272	71.5	5.1	277	2	US-09-303-518D-402	Sequence 402, App	345	71	5.1	594	2	US-09-650-324A-59	Sequence 59, Appl
273	71.5	5.1	287	2	US-09-134-001C-5055	Sequence 5055, Ap	346	71	5.1	594	2	US-10-039-112A-59	Sequence 59, Appl
274	71.5	5.1	292	2	US-09-489-039A-12212	Sequence 12212, A	347	71	5.1	627	2	US-09-902-540-15743	Sequence 15743, A
275	71.5	5.1	309	3	US-10-770-127-22	Sequence 22, Appl	348	71	5.1	658	1	US-08-825-558-4	Sequence 4, Appli
276	71.5	5.1	372	1	US-08-501-003A-12	Sequence 12, Appl	349	71	5.1	658	2	US-09-312-611-4	Sequence 4, Appli
277	71.5	5.1	379	2	US-09-740-035-4	Sequence 4, Appli	350	71	5.1	693	2	US-09-999-833A-483	Sequence 483, App
278	71.5	5.1	379	2	US-10-056-790-8	Sequence 8, Appli	351	71	5.1	693	2	US-10-020-445A-483	Sequence 483, App
279	71.5	5.1	379	2	US-10-056-790-40	Sequence 40, Appl	352	71	5.1	693	2	US-09-978-189-483	Sequence 483, App
280	71.5	5.1	383	1	US-08-501-003A-14	Sequence 14, Appl	353	71	5.1	693	2	US-10-017-085A-483	Sequence 483, App
281	71.5	5.1	389	1	US-08-501-003A-11	Sequence 11, Appl	354	71	5.1	693	3	US-10-145-129A-483	Sequence 483, App
282	71.5	5.1	391	1	US-08-501-003A-13	Sequence 13, Appl	355	71	5.1	693	3	US-10-013-929A-483	Sequence 483, App
283	71.5	5.1	391	2	US-09-949-016-5904	Sequence 5904, Ap	356	71	5.1	693	3	US-10-013-917A-483	Sequence 483, App
284	71.5	5.1	398	1	US-08-501-003A-15	Sequence 15, Appl	357	71	5.1	859	2	US-09-313-942-7	Sequence 7, Appli
285	71.5	5.1	411	2	US-09-949-016-8100	Sequence 8100, Ap	358	71	5.1	859	2	US-10-282-162-7	Sequence 7, Appli
286	71.5	5.1	412	2	US-10-138-701-59	Sequence 59, Appl	359	71	5.1	918	1	US-08-825-558-6	Sequence 6, Appli
287	71.5	5.1	484	2	US-09-248-796A-20357	Sequence 20357, A	360	71	5.1	918	2	US-09-312-611-6	Sequence 6, Appli
288	71.5	5.1	519	2	US-09-198-452A-561	Sequence 561, App	361	71	5.1	918	2	US-09-853-180B-3	Sequence 3, Appli
289	71.5	5.1	521	2	US-09-438-185A-523	Sequence 523, App	362	71	5.1	918	2	US-09-949-002-333	Sequence 333, App
290	71.5	5.1	535	2	US-09-252-991A-21652	Sequence 21652, A	363	71	5.1	922	2	US-09-569-611C-41	Sequence 41, Appl
291	71.5	5.1	552	2	US-09-270-767-45540	Sequence 45540, A	364	71	5.1	951	2	US-09-313-942-9	Sequence 9, Appli
292	71.5	5.1	574	2	US-09-248-796A-20132	Sequence 20132, A	365	71	5.1	951	2	US-10-282-162-9	Sequence 9, Appli
293	71.5	5.1	587	2	US-08-635-552A-3	Sequence 3, Appli	366	71	5.1	971	2	US-09-868-572A-1	Sequence 1, Appli
294	71	5.1	201	2	US-09-270-767-33463	Sequence 33463, A	367	70.5	5.1	150	2	US-09-134-000C-4337	Sequence 4337, Ap
295	71	5.1	201	2	US-09-270-767-48680	Sequence 48680, A	368	70.5	5.1	286	2	US-09-248-796A-17897	Sequence 17897, A
296	71	5.1	261	2	US-10-012-231A-326	Sequence 326, App	369	70.5	5.1	319	2	US-09-130-749-2	Sequence 2, Appli
297	71	5.1	261	2	US-10-015-389A-326	Sequence 326, App	370	70.5	5.1	319	2	US-09-130-749-2	Sequence 2, Appli
298	71	5.1	261	2	US-10-006-768A-326	Sequence 326, App	371	70.5	5.1	319	2	US-09-170-496D-60	Sequence 60, Appl
299	71	5.1	261	2	US-10-015-671A-326	Sequence 326, App	372	70.5	5.1	386	2	US-09-949-016-10000	Sequence 10000, A
300	71	5.1	261	2	US-10-015-393A-326	Sequence 326, App	373	70.5	5.1	387	2	US-09-489-039A-12240	Sequence 12240, A
301	71	5.1	261	2	US-10-011-833A-326	Sequence 326, App	374	70.5	5.1	395	2	US-09-543-681A-6203	Sequence 6203, Ap
302	71	5.1	261	2	US-10-012-064A-326	Sequence 326, App	375	70.5	5.1	399	2	US-09-489-039A-8272	Sequence 8272, Ap
303	71	5.1	261	2	US-10-012-064A-326	Sequence 326, App	376	70.5	5.1	420	2	US-09-134-001C-3805	Sequence 3805, Ap
304	71	5.1	261	2	US-10-015-392A-326	Sequence 326, App	377	70.5	5.1	443	2	US-09-489-039A-8166	Sequence 8166, Ap
305	71	5.1	261	3	US-10-011-795B-326	Sequence 326, App	378	70.5	5.1	444	2	US-09-328-352-5249	Sequence 5249, Ap
306	71	5.1	261	3	US-10-015-386A-326	Sequence 326, App	379	70.5	5.1	454	1	US-08-748-485-1	Sequence 1, Appli
307	71	5.1	261	3	US-10-012-121A-326	Sequence 326, App	380	70.5	5.1	467	2	US-09-107-532A-6175	Sequence 6175, Ap
308	71	5.1	261	3	US-10-006-485A-326	Sequence 326, App	381	70.5	5.1	472	2	US-09-934-899-10	Sequence 10, Appl
309	71	5.1	261	3	US-10-006-746A-326	Sequence 326, App	382	70.5	5.1	472	2	US-09-934-868-30	Sequence 30, Appl
310	71	5.1	261	3	US-10-012-752A-326	Sequence 326, App	383	70.5	5.1	472	2	US-10-701-200-30	Sequence 30, Appl
311	71	5.1	261	3	US-10-017-253A-326	Sequence 326, App	384	70.5	5.1	473	2	US-09-949-016-11735	Sequence 11735, A
312	71	5.1	261	3	US-10-015-519A-326	Sequence 326, App	385	70.5	5.1	474	2	US-09-486-192-4	Sequence 4, Appli
313	71	5.1	261	3	US-10-015-715A-326	Sequence 326, App	386	70.5	5.1	474	2	US-10-328-459A-4	Sequence 4, Appli
314	71	5.1	261	3	US-10-007-236A-326	Sequence 326, App	387	70.5	5.1	500	2	US-09-489-039A-10995	Sequence 10995, A
315	71	5.1	332	2	US-09-313-942-10	Sequence 10, Appl	388	70.5	5.1	619	2	US-09-248-796A-20837	Sequence 20837, A
316	71	5.1	332	2	US-10-282-162-10	Sequence 10, Appl	389	70.5	5.1	659	2	US-09-949-016-6720	Sequence 6720, Ap
317	71	5.1	347	2	US-09-769-787-20	Sequence 20, Appl	390	70.5	5.1	681	2	US-09-248-796A-20121	Sequence 20121, A
318	71	5.1	369	2	US-09-838-955A-3	Sequence 3, Appli	391	70.5	5.1	687	3	US-10-179-410-2	Sequence 2, Appli

392	70.5	5.1	877	1	US-08-072-574-12	Sequence 12, Appl	465	69	5.0	308	2	US-09-438-185A-569	Sequence 569, App
393	70.5	5.1	955	2	US-09-252-991A-18882	Sequence 18882, A	466	69	5.0	309	2	US-10-111-105B-2	Sequence 2, Appli
394	70.5	5.1	1134	2	US-08-726-214-2	Sequence 2, Appli	467	69	5.0	316	1	US-08-827-291A-2	Sequence 2, Appli
395	70.5	5.1	1134	2	US-09-245-039-2	Sequence 2, Appli	468	69	5.0	321	2	US-10-314-048A-10	Sequence 10, Appl
396	70.5	5.1	1681	2	US-09-920-653B-3	Sequence 3, Appli	469	69	5.0	344	2	US-10-121-757B-20	Sequence 20, Appl
397	70.5	5.1	1788	1	US-08-962-284-2	Sequence 2, Appli	470	69	5.0	359	2	US-09-875-076-28	Sequence 28, Appl
398	70	5.0	139	2	US-09-489-039A-8585	Sequence 8585, Ap	471	69	5.0	380	1	US-08-227-108-16	Sequence 16, Appl
399	70	5.0	235	2	US-09-252-991A-19945	Sequence 19945, A	472	69	5.0	380	1	US-09-073-674-16	Sequence 16, Appl
400	70	5.0	296	2	US-09-328-352-7482	Sequence 7482, Ap	473	69	5.0	397	2	US-09-328-352-7357	Sequence 7357, Ap
401	70	5.0	314	2	US-09-543-681A-6497	Sequence 6497, Ap	474	69	5.0	403	2	US-09-489-039A-9921	Sequence 9921, Ap
402	70	5.0	429	2	US-09-156-809-1	Sequence 1, Appli	475	69	5.0	420	2	US-09-328-352-5907	Sequence 5907, Ap
403	70	5.0	429	2	US-10-006-915-1	Sequence 1, Appli	476	69	5.0	446	2	US-09-248-796A-20349	Sequence 20349, A
404	70	5.0	492	2	US-09-328-352-6875	Sequence 6875, Ap	477	69	5.0	451	2	US-09-303-518D-150	Sequence 150, App
405	70	5.0	496	2	US-09-489-039A-8772	Sequence 8772, Ap	478	69	5.0	451	2	US-09-303-518D-152	Sequence 152, App
406	70	5.0	502	2	US-08-771-737-2	Sequence 2, Appli	479	69	5.0	466	2	US-09-762-278-2	Sequence 2, Appli
407	70	5.0	502	2	US-09-954-936-2	Sequence 2, Appli	480	69	5.0	483	2	US-09-134-000C-4234	Sequence 4234, Ap
408	70	5.0	526	2	US-09-543-681A-6494	Sequence 6494, Ap	481	69	5.0	506	2	US-09-540-236-2360	Sequence 2360, Ap
409	70	5.0	535	2	US-09-252-991A-21805	Sequence 21805, A	482	69	5.0	520	2	US-09-248-796A-20803	Sequence 20803, A
410	70	5.0	539	2	US-09-538-092-741	Sequence 741, App	483	69	5.0	583	2	US-09-489-039A-13918	Sequence 13918, A
411	70	5.0	560	2	US-09-999-833A-420	Sequence 420, App	484	69	5.0	642	2	US-09-252-991A-23588	Sequence 23588, A
412	70	5.0	560	2	US-10-020-445A-420	Sequence 420, App	485	69	5.0	719	2	US-09-328-352-6274	Sequence 6274, Ap
413	70	5.0	560	2	US-09-978-189-420	Sequence 420, App	486	69	5.0	852	2	US-09-254-344-4	Sequence 4, Appli
414	70	5.0	560	2	US-10-017-085A-420	Sequence 420, App	487	69	5.0	854	2	US-09-254-352B-18	Sequence 18, Appl
415	70	5.0	560	3	US-10-145-129A-420	Sequence 420, App	488	69	5.0	934	1	US-08-215-805A-80	Sequence 80, Appl
416	70	5.0	560	3	US-10-013-929A-420	Sequence 420, App	489	69	5.0	1095	2	US-09-112-096-15	Sequence 15, Appl
417	70	5.0	560	3	US-10-013-917A-420	Sequence 420, App	490	69	5.0	1095	2	US-09-636-215-778	Sequence 778, App
418	70	5.0	594	2	US-09-489-039A-10622	Sequence 10622, A	491	69	5.0	1095	2	US-09-685-166A-778	Sequence 778, App
419	70	5.0	688	2	US-09-438-185A-870	Sequence 870, App	492	69	5.0	1095	2	US-09-679-426-778	Sequence 778, App
420	70	5.0	708	1	US-07-797-556-2	Sequence 2, Appli	493	69	5.0	1095	2	US-09-759-143-778	Sequence 778, App
421	70	5.0	708	1	US-08-308-881-2	Sequence 2, Appli	494	69	5.0	1095	2	US-09-651-236-778	Sequence 778, App
422	70	5.0	708	1	US-09-058-263-2	Sequence 2, Appli	495	69	5.0	1095	2	US-09-657-279-778	Sequence 778, App
423	70	5.0	708	1	US-09-059-099-2	Sequence 2, Appli	496	69	5.0	1095	2	US-10-012-896-778	Sequence 778, App
424	70	5.0	708	2	US-09-058-264-2	Sequence 2, Appli	497	69	5.0	1095	3	US-10-144-678A-778	Sequence 778, App
425	70	5.0	708	2	US-09-455-962-2	Sequence 2, Appli	498	69	5.0	1180	1	US-08-072-574-8	Sequence 8, Appli
426	70	5.0	708	5	PCT-US95-06530-2	Sequence 2, Appli	499	69	5.0	1212	1	US-08-072-574-10	Sequence 10, Appl
427	70	5.0	1028	2	US-09-328-352-5749	Sequence 5749, Ap	500	69	5.0	2037	2	US-09-543-681A-5538	Sequence 5538, Ap
428	70	5.0	1165	2	US-09-949-016-6874	Sequence 6874, Ap	501	69	5.0	2873	1	US-08-466-033-15	Sequence 15, Appl
429	70	5.0	1165	2	US-09-949-016-11392	Sequence 11392, A	502	69	5.0	2873	1	US-08-638-911A-2	Sequence 2, Appli
430	70	5.0	2105	1	US-08-808-793-3	Sequence 3, Appli	503	69	5.0	2873	1	US-08-444-733-15	Sequence 15, Appl
431	70	5.0	2105	2	US-08-772-512A-3	Sequence 3, Appli	504	69	5.0	2873	1	US-08-461-361-15	Sequence 15, Appl
432	70	5.0	2105	2	US-09-428-371-3	Sequence 3, Appli	505	69	5.0	2873	1	US-08-485-910-15	Sequence 15, Appl
433	69.5	5.0	293	2	US-09-902-540-11200	Sequence 11200, A	506	69	5.0	2873	1	US-08-485-910-15	Sequence 15, Appl
434	69.5	5.0	308	2	US-09-595-386-3	Sequence 3, Appli	507	69	5.0	2873	5	PCT-US95-06266-15	Sequence 15, Appl
435	69.5	5.0	308	2	US-09-993-525-3	Sequence 3, Appli	508	68.5	4.9	180	2	US-09-270-767-32589	Sequence 32589, A
436	69.5	5.0	345	2	US-09-543-681A-7546	Sequence 7546, Ap	509	68.5	4.9	180	2	US-09-270-767-47806	Sequence 47806, A
437	69.5	5.0	350	2	US-09-540-236-2338	Sequence 2338, Ap	510	68.5	4.9	241	1	US-08-825-781-3	Sequence 3, Appli
438	69.5	5.0	406	2	US-09-328-352-7149	Sequence 7149, Ap	511	68.5	4.9	264	2	US-09-724-864-64	Sequence 64, Appl
439	69.5	5.0	417	2	US-09-405-558-44	Sequence 44, Appl	512	68.5	4.9	300	2	US-09-489-039A-10701	Sequence 10701, A
440	69.5	5.0	417	2	US-09-538-036-44	Sequence 44, Appl	513	68.5	4.9	346	2	US-10-152-886-91	Sequence 91, Appl
441	69.5	5.0	424	3	US-09-802-208B-5	Sequence 5, Appli	514	68.5	4.9	365	2	US-09-902-540-14946	Sequence 14946, A
442	69.5	5.0	456	2	US-09-489-039A-8332	Sequence 8332, Ap	515	68.5	4.9	396	2	US-09-107-532A-4277	Sequence 4277, Ap
443	69.5	5.0	460	2	US-09-489-039A-13505	Sequence 13505, A	516	68.5	4.9	400	2	US-09-134-001C-2912	Sequence 2912, Ap
444	69.5	5.0	472	2	US-10-154-419-79	Sequence 79, Appl	517	68.5	4.9	405	2	US-09-543-681A-6109	Sequence 6109, Ap
445	69.5	5.0	493	1	US-08-362-512A-4	Sequence 4, Appli	518	68.5	4.9	412	2	US-09-134-001C-4885	Sequence 4885, Ap
446	69.5	5.0	493	2	US-08-964-939-4	Sequence 4, Appli	519	68.5	4.9	427	2	US-09-252-991A-29948	Sequence 29948, A
447	69.5	5.0	493	2	US-08-854-774-4	Sequence 4, Appli	520	68.5	4.9	428	2	US-09-328-352-5543	Sequence 5543, Ap
448	69.5	5.0	501	2	US-09-252-991A-28456	Sequence 28456, A	521	68.5	4.9	459	2	US-09-583-110-5017	Sequence 5017, Ap
449	69.5	5.0	513	1	US-09-122-230-7	Sequence 7, Appli	522	68.5	4.9	459	2	US-09-769-787-85	Sequence 85, Appl
450	69.5	5.0	530	2	US-09-540-236-2483	Sequence 2483, Ap	523	68.5	4.9	465	2	US-09-489-039A-7435	Sequence 7435, Ap
451	69.5	5.0	591	2	US-09-643-657-15	Sequence 15, Appl	524	68.5	4.9	470	2	US-09-107-433-4341	Sequence 4341, Ap
452	69.5	5.0	627	2	US-09-538-092-760	Sequence 760, App	525	68.5	4.9	480	2	US-09-305-681-2	Sequence 2, Appli
453	69.5	5.0	653	1	US-07-782-298-2	Sequence 2, Appli	526	68.5	4.9	487	2	US-09-911-132A-4	Sequence 4, Appli
454	69.5	5.0	688	2	US-09-543-681A-4896	Sequence 4896, Ap	527	68.5	4.9	511	2	US-09-305-681-6	Sequence 6, Appli
455	69.5	5.0	1277	2	US-09-397-885-3	Sequence 3, Appli	528	68.5	4.9	538	2	US-09-252-991A-23060	Sequence 23060, A
456	69.5	5.0	1277	2	US-09-969-362-3	Sequence 3, Appli	529	68.5	4.9	541	2	US-09-976-594-931	Sequence 931, App
457	69	5.0	114	2	US-09-134-001C-3376	Sequence 3376, Ap	530	68.5	4.9	549	2	US-09-248-796A-20436	Sequence 20436, A
458	69	5.0	201	2	US-09-605-703B-1952	Sequence 1952, Ap	531	68.5	4.9	661	3	US-10-114-270-142	Sequence 142, App
459	69	5.0	241	2	US-09-328-352-7032	Sequence 7032, Ap	532	68.5	4.9	716	2	US-09-303-518D-108	Sequence 108, App
460	69	5.0	292	2	US-09-270-767-41753	Sequence 41753, A	533	68.5	4.9	1091	2	US-09-925-388-7	Sequence 7, Appli
461	69	5.0	293	2	US-09-438-185A-313	Sequence 313, App	534	68.5	4.9	1091	2	US-09-306-595C-7	Sequence 7, Appli
462	69	5.0	294	2	US-09-902-540-11124	Sequence 11124, A	535	68.5	4.9	1091	2	US-10-431-846-7	Sequence 7, Appli
463	69	5.0	307	2	US-09-605-703B-2582	Sequence 2582, Ap	536	68.5	4.9	2104	1	US-08-808-793-4	Sequence 4, Appli
464	69	5.0	308	2	US-09-198-452A-606	Sequence 606, App	537	68.5	4.9	2104	2	US-08-772-512A-4	Sequence 4, Appli



538	68.5	4.9	2104	2	US-09-428-371-4	Sequence 4, Appli	611	67.5	4.8	940	2	US-09-328-352-8165	Sequence 8165, Ap
539	68.5	4.9	3559	2	US-09-693-205A-10	Sequence 10, Appl	612	67.5	4.8	1084	2	US-09-221-013A-8	Sequence 8, Appli
540	68	4.9	253	2	US-08-858-207A-299	Sequence 299, App	613	67.5	4.8	1326	2	US-09-328-352-4886	Sequence 4886, Ap
541	68	4.9	279	2	US-09-602-787A-658	Sequence 658, App	614	67	4.8	148	2	US-09-270-767-39883	Sequence 39883, A
542	68	4.9	309	2	US-09-710-279-42	Sequence 42, Appl	615	67	4.8	148	2	US-09-270-767-55100	Sequence 55100, A
543	68	4.9	313	2	US-09-583-110-4236	Sequence 4236, Ap	616	67	4.8	162	2	US-09-270-767-45268	Sequence 45268, A
544	68	4.9	315	2	US-09-107-433-3706	Sequence 3706, Ap	617	67	4.8	184	2	US-09-795-926-46	Sequence 46, Appl
545	68	4.9	355	2	US-09-826-509-475	Sequence 475, App	618	67	4.8	184	2	US-10-364-774-46	Sequence 46, Appl
546	68	4.9	379	2	US-09-252-991A-27854	Sequence 27854, A	619	67	4.8	205	2	US-09-252-991A-28363	Sequence 28363, A
547	68	4.9	404	2	US-09-328-352-8182	Sequence 8182, Ap	620	67	4.8	217	2	US-09-134-000C-6287	Sequence 6287, Ap
548	68	4.9	466	2	US-09-603-208A-236	Sequence 236, App	621	67	4.8	217	4	US-10-038-895A-7	Sequence 7, Appli
549	68	4.9	470	2	US-09-328-352-6673	Sequence 6673, Ap	622	67	4.8	225	2	US-09-543-681A-7698	Sequence 7698, Ap
550	68	4.9	476	2	US-09-328-352-6735	Sequence 6735, Ap	623	67	4.8	277	2	US-09-489-039A-10481	Sequence 10481, A
551	68	4.9	484	2	US-09-134-001C-5063	Sequence 5063, Ap	624	67	4.8	290	2	US-09-248-796A-20347	Sequence 20347, A
552	68	4.9	486	2	US-09-134-001C-3593	Sequence 3593, Ap	625	67	4.8	306	2	US-09-489-039A-10023	Sequence 10023, A
553	68	4.9	503	2	US-09-248-796A-16650	Sequence 16650, A	626	67	4.8	326	2	US-09-543-681A-6673	Sequence 6673, Ap
554	68	4.9	548	2	US-09-328-352-6605	Sequence 6605, Ap	627	67	4.8	345	2	US-09-248-796A-20118	Sequence 20118, A
555	68	4.9	605	2	US-09-583-110-4773	Sequence 4773, Ap	628	67	4.8	359	2	US-09-425-488-2	Sequence 2, Appli
556	68	4.9	619	2	US-09-540-236-2377	Sequence 2377, Ap	629	67	4.8	360	2	US-09-489-039A-8125	Sequence 8125, Ap
557	68	4.9	633	2	US-09-328-352-5439	Sequence 5439, Ap	630	67	4.8	375	2	US-09-543-681A-4465	Sequence 4465, Ap
558	68	4.9	638	1	US-08-295-814E-13	Sequence 13, Appl	631	67	4.8	382	2	US-09-489-039A-10783	Sequence 10783, A
559	68	4.9	638	1	US-08-240-783B-2	Sequence 2, Appli	632	67	4.8	414	2	US-09-334-601-4	Sequence 4, Appli
560	68	4.9	638	2	US-09-084-813-2	Sequence 2, Appli	633	67	4.8	453	1	US-08-439-131A-5	Sequence 5, Appli
561	68	4.9	638	2	US-09-343-361-13	Sequence 13, Appl	634	67	4.8	453	1	US-08-440-674-4	Sequence 4, Appli
562	68	4.9	638	5	PCT-US92-09662-2	Sequence 2, Appli	635	67	4.8	453	2	US-08-879-337-6	Sequence 6, Appli
563	68	4.9	640	2	US-09-627-376-16	Sequence 16, Appl	636	67	4.8	459	2	US-09-097-889-22	Sequence 22, Appl
564	68	4.9	640	2	US-10-047-676B-16	Sequence 16, Appl	637	67	4.8	459	2	US-09-098-079-22	Sequence 22, Appl
565	68	4.9	672	2	US-09-543-681A-5976	Sequence 5976, Ap	638	67	4.8	465	2	US-09-252-991A-19135	Sequence 19135, A
566	68	4.9	694	2	US-09-248-796A-20210	Sequence 20210, A	639	67	4.8	482	2	US-09-489-039A-9369	Sequence 9369, Ap
567	68	4.9	727	2	US-09-543-681A-6690	Sequence 6690, Ap	640	67	4.8	490	2	US-09-328-352-5310	Sequence 5310, Ap
568	68	4.9	783	2	US-09-165-396-2	Sequence 2, Appli	641	67	4.8	494	2	US-09-489-039A-8154	Sequence 8154, Ap
569	68	4.9	905	2	US-09-538-092-1079	Sequence 1079, Ap	642	67	4.8	505	2	US-09-328-352-7155	Sequence 7155, Ap
570	68	4.9	1024	2	US-09-562-737-87	Sequence 87, Appl	643	67	4.8	506	2	US-09-134-000C-6170	Sequence 6170, Ap
571	68	4.9	2864	2	US-08-469-260A-394	Sequence 394, App	644	67	4.8	519	2	US-09-719-919A-17	Sequence 17, Appl
572	68	4.9	2864	2	US-08-488-446-394	Sequence 394, App	645	67	4.8	541	2	US-09-716-129-54	Sequence 54, Appl
573	68	4.9	2864	2	US-08-467-344A-394	Sequence 394, App	646	67	4.8	545	2	US-09-902-540-10576	Sequence 10576, A
574	68	4.9	2864	2	US-08-424-550B-394	Sequence 394, App	647	67	4.8	548	2	US-09-543-681A-4994	Sequence 4994, Ap
575	67.5	4.8	181	2	US-09-270-767-33574	Sequence 33574, A	648	67	4.8	576	2	US-09-540-236-2286	Sequence 2286, Ap
576	67.5	4.8	196	2	US-09-383-586-11	Sequence 11, Appl	649	67	4.8	590	2	US-09-902-540-14944	Sequence 14944, A
577	67.5	4.8	196	2	US-09-823-038A-11	Sequence 11, Appl	650	67	4.8	601	2	US-09-134-000C-5783	Sequence 5783, Ap
578	67.5	4.8	240	2	US-09-540-236-2487	Sequence 2487, Ap	651	67	4.8	768	2	US-09-489-039A-12897	Sequence 12897, A
579	67.5	4.8	249	2	US-09-949-016-7192	Sequence 7192, Ap	652	67	4.8	774	2	US-09-328-352-5361	Sequence 5361, Ap
580	67.5	4.8	264	2	US-09-270-767-41787	Sequence 41787, A	653	67	4.8	878	2	US-10-169-048-42	Sequence 42, Appl
581	67.5	4.8	265	2	US-09-248-796A-17984	Sequence 17984, A	654	67	4.8	1439	1	US-08-449-644-2	Sequence 2, Appli
582	67.5	4.8	299	3	US-10-770-127-139	Sequence 139, App	655	67	4.8	1439	1	US-08-087-244A-2	Sequence 2, Appli
583	67.5	4.8	304	2	US-09-328-352-6103	Sequence 6103, Ap	656	67	4.8	1457	1	US-08-652-971-3	Sequence 3, Appli
584	67.5	4.8	317	2	US-09-489-039A-9602	Sequence 9602, Ap	657	67	4.8	1457	1	US-08-449-644-1	Sequence 1, Appli
585	67.5	4.8	323	2	US-09-107-532A-5460	Sequence 5460, Ap	658	67	4.8	1457	1	US-08-087-244A-1	Sequence 1, Appli
586	67.5	4.8	327	2	US-09-543-681A-6219	Sequence 6219, Ap	659	67	4.8	1457	1	US-08-991-258A-3	Sequence 3, Appli
587	67.5	4.8	336	1	US-08-332-312-4	Sequence 4, Appli	660	67	4.8	1457	1	US-08-769-399-3	Sequence 3, Appli
588	67.5	4.8	360	2	US-09-949-016-10048	Sequence 10048, A	661	67	4.8	1457	2	US-08-991-953A-3	Sequence 3, Appli
589	67.5	4.8	370	2	US-09-303-518D-110	Sequence 110, App	662	66.5	4.8	175	2	US-09-583-110-4664	Sequence 4664, Ap
590	67.5	4.8	411	2	US-09-328-352-5039	Sequence 5039, Ap	663	66.5	4.8	175	2	US-09-769-787-97	Sequence 97, Appl
591	67.5	4.8	421	2	US-09-198-452A-932	Sequence 932, App	664	66.5	4.8	179	2	US-09-107-433-4882	Sequence 4882, Ap
592	67.5	4.8	421	2	US-09-438-185A-869	Sequence 869, App	665	66.5	4.8	243	2	US-09-134-001C-4114	Sequence 4114, Ap
593	67.5	4.8	425	2	US-09-134-000C-5971	Sequence 5971, Ap	666	66.5	4.8	249	2	US-08-858-207A-309	Sequence 309, App
594	67.5	4.8	484	2	US-09-252-991A-32299	Sequence 32299, A	667	66.5	4.8	249	2	US-09-270-767-38186	Sequence 38186, A
595	67.5	4.8	536	2	US-09-107-532A-5507	Sequence 5507, Ap	668	66.5	4.8	249	2	US-09-270-767-53403	Sequence 53403, A
596	67.5	4.8	586	2	US-09-252-991A-24994	Sequence 24994, A	669	66.5	4.8	256	2	US-09-489-039A-9057	Sequence 9057, Ap
597	67.5	4.8	612	2	US-09-248-796A-18040	Sequence 18040, A	670	66.5	4.8	274	2	US-09-830-230A-190	Sequence 190, App
598	67.5	4.8	625	2	US-09-902-540-15330	Sequence 15330, A	671	66.5	4.8	300	2	US-09-393-634-19	Sequence 19, Appl
599	67.5	4.8	632	2	US-09-949-016-10386	Sequence 10386, A	672	66.5	4.8	300	3	US-10-770-127-113	Sequence 113, App
600	67.5	4.8	662	2	US-09-583-110-5119	Sequence 5119, Ap	673	66.5	4.8	306	2	US-09-830-230A-189	Sequence 189, App
601	67.5	4.8	664	2	US-09-107-433-2775	Sequence 2775, Ap	674	66.5	4.8	319	2	US-09-170-496D-196	Sequence 196, App
602	67.5	4.8	667	1	US-07-879-617A-8	Sequence 8, Appli	675	66.5	4.8	324	2	US-09-543-681A-6241	Sequence 6241, Ap
603	67.5	4.8	667	1	US-08-753-985-8	Sequence 18, Appli	676	66.5	4.8	343	2	US-09-491-577-96	Sequence 96, Appl
604	67.5	4.8	680	2	US-09-720-317A-18	Sequence 18, Appli	677	66.5	4.8	349	2	US-09-543-681A-6853	Sequence 6853, Ap
605	67.5	4.8	693	2	US-09-949-016-9666	Sequence 9666, Ap	678	66.5	4.8	380	2	US-09-949-016-10856	Sequence 10856, A
606	67.5	4.8	716	2	US-09-303-518D-112	Sequence 112, App	679	66.5	4.8	392	2	US-09-603-208A-134	Sequence 134, App
607	67.5	4.8	767	2	US-09-328-352-4613	Sequence 4613, Ap	680	66.5	4.8	412	2	US-09-710-279-368	Sequence 368, App
608	67.5	4.8	912	2	US-08-617-785-2	Sequence 2, Appli	681	66.5	4.8	414	2	US-09-605-703B-2352	Sequence 2352, Ap
609	67.5	4.8	912	2	US-09-641-318-2	Sequence 2, Appli	682	66.5	4.8	415	2	US-09-489-039A-10457	Sequence 10457, A
610	67.5	4.8	912	2	US-09-817-464-2	Sequence 2, Appli	683	66.5	4.8	425	2	US-09-543-681A-7042	Sequence 7042, Ap

684	66.5	4.8	430	2	US-10-104-047-2265	Sequence 2265, Ap	757	66	4.7	511	2	US-08-471-961-8	Sequence 8, Appli
685	66.5	4.8	444	2	US-09-694-519-6	Sequence 6, Appli	758	66	4.7	511	2	US-09-345-109C-8	Sequence 8, Appli
686	66.5	4.8	456	2	US-09-328-352-5446	Sequence 5446, Ap	759	66	4.7	536	2	US-09-270-767-44004	Sequence 44004, A
687	66.5	4.8	470	1	US-08-959-011-1	Sequence 1, Appli	760	66	4.7	619	2	US-09-578-441-3	Sequence 3, Appli
688	66.5	4.8	488	2	US-09-801-052-5	Sequence 5, Appli	761	66	4.7	620	2	US-09-578-441-4	Sequence 4, Appli
689	66.5	4.8	488	2	US-10-020-121-5	Sequence 5, Appli	762	66	4.7	639	2	US-09-134-001C-5661	Sequence 5661, Ap
690	66.5	4.8	488	2	US-10-636-579-5	Sequence 5, Appli	763	66	4.7	687	2	US-08-834-467-2	Sequence 2, Appli
691	66.5	4.8	503	2	US-09-920-262A-9	Sequence 9, Appli	764	66	4.7	687	2	US-09-396-177-2	Sequence 2, Appli
692	66.5	4.8	511	2	US-09-328-352-6365	Sequence 6365, Ap	765	66	4.7	687	2	US-09-248-796A-14715	Sequence 14715, A
693	66.5	4.8	515	2	US-09-489-039A-8402	Sequence 8402, Ap	766	66	4.7	748	2	US-09-902-540-13877	Sequence 13877, A
694	66.5	4.8	525	2	US-09-252-991A-23870	Sequence 23870, A	767	66	4.7	856	2	US-10-034-749-2929	Sequence 2929, Ap
695	66.5	4.8	534	2	US-09-107-532A-6592	Sequence 6592, Ap	768	66	4.7	986	2	US-09-248-796A-19088	Sequence 19088, A
696	66.5	4.8	535	2	US-09-107-532A-6593	Sequence 6593, Ap	769	66	4.7	1078	2	US-10-125-772-28	Sequence 28, Appl
697	66.5	4.8	536	2	US-09-809-665A-71	Sequence 71, Appl	770	66	4.7	1078	2	US-10-125-778-28	Sequence 28, Appl
698	66.5	4.8	595	2	US-10-104-047-2714	Sequence 2714, Ap	771	66	4.7	1078	2	US-10-125-792-28	Sequence 28, Appl
699	66.5	4.8	598	2	US-09-107-532A-7027	Sequence 7027, Ap	772	66	4.7	1216	2	US-09-248-796A-19646	Sequence 19646, A
700	66.5	4.8	648	2	US-09-583-110-2729	Sequence 2729, Ap	773	66	4.7	1724	2	US-09-964-899-43	Sequence 43, Appl
701	66.5	4.8	670	2	US-09-107-433-4919	Sequence 4919, Ap	774	66	4.7	4377	2	US-09-949-016-6978	Sequence 6978, Ap
702	66.5	4.8	676	2	US-09-198-452A-836	Sequence 836, App	775	65.5	4.7	157	2	US-09-461-325-155	Sequence 155, App
703	66.5	4.8	688	2	US-09-720-317A-2	Sequence 2, Appli	776	65.5	4.7	157	2	US-10-012-542-155	Sequence 155, App
704	66.5	4.8	719	2	US-09-438-185A-788	Sequence 788, App	777	65.5	4.7	157	2	US-10-115-123-155	Sequence 155, App
705	66.5	4.8	736	2	US-09-107-532A-6007	Sequence 6007, Ap	778	65.5	4.7	160	2	US-09-270-767-46920	Sequence 46920, A
706	66.5	4.8	737	2	US-09-583-110-4038	Sequence 4038, Ap	779	65.5	4.7	195	2	US-09-489-039A-7897	Sequence 7897, Ap
707	66.5	4.8	738	2	US-09-328-352-4315	Sequence 4315, Ap	780	65.5	4.7	239	2	US-09-830-230A-242	Sequence 242, App
708	66.5	4.8	742	2	US-09-107-433-3626	Sequence 3626, Ap	781	65.5	4.7	267	2	US-09-198-452A-231	Sequence 231, App
709	66.5	4.8	755	2	US-09-489-039A-9089	Sequence 9089, Ap	782	65.5	4.7	270	2	US-09-270-767-44001	Sequence 44001, A
710	66.5	4.8	865	2	US-09-252-991A-19339	Sequence 19339, A	783	65.5	4.7	273	2	US-09-830-230A-241	Sequence 241, App
711	66.5	4.8	899	2	US-09-437-568A-48	Sequence 48, Appl	784	65.5	4.7	292	2	US-09-372-422A-4	Sequence 4, Appli
712	66.5	4.8	921	1	US-07-718-575-14	Sequence 14, Appl	785	65.5	4.7	300	2	US-09-303-518D-542	Sequence 542, App
713	66.5	4.8	921	1	US-08-481-206-14	Sequence 14, Appl	786	65.5	4.7	305	2	US-09-107-433-3400	Sequence 3400, Ap
714	66.5	4.8	921	1	US-08-486-269A-14	Sequence 14, Appl	787	65.5	4.7	310	2	US-09-328-352-8117	Sequence 8117, Ap
715	66.5	4.8	1059	2	US-10-160-719A-2	Sequence 2, Appli	788	65.5	4.7	323	2	US-09-134-001C-4635	Sequence 4635, Ap
716	66.5	4.8	1059	2	US-10-209-059-42	Sequence 42, Appl	789	65.5	4.7	329	2	US-09-740-035-2	Sequence 2, Appli
717	66.5	4.8	1148	2	US-09-900-237-4	Sequence 4, Appli	790	65.5	4.7	329	2	US-09-710-279-1942	Sequence 1942, Ap
718	66.5	4.8	1167	2	US-09-008-697-6	Sequence 6, Appli	791	65.5	4.7	332	3	US-10-770-127-101	Sequence 101, App
719	66.5	4.8	1167	2	US-09-472-667-6	Sequence 6, Appli	792	65.5	4.7	344	2	US-09-134-001C-5567	Sequence 5567, Ap
720	66.5	4.8	1548	2	US-10-418-036-14	Sequence 14, Appl	793	65.5	4.7	355	1	US-08-153-848-28	Sequence 28, Appl
721	66.5	4.8	1684	2	US-08-665-259-25	Sequence 25, Appl	794	65.5	4.7	355	1	US-08-153-848-32	Sequence 32, Appl
722	66.5	4.8	1684	2	US-08-762-500-25	Sequence 25, Appl	795	65.5	4.7	355	2	US-09-299-843A-28	Sequence 28, Appl
723	66.5	4.8	1704	2	US-08-762-500-75	Sequence 75, Appl	796	65.5	4.7	355	2	US-09-299-843A-32	Sequence 32, Appl
724	66.5	4.8	1704	2	US-09-032-438C-120	Sequence 120, App	797	65.5	4.7	355	2	US-09-088-337B-28	Sequence 28, Appl
725	66.5	4.8	1766	2	US-09-949-016-10796	Sequence 10796, A	798	65.5	4.7	355	2	US-09-088-337B-32	Sequence 32, Appl
726	66	4.7	171	2	US-09-107-383-16	Sequence 16, Appl	799	65.5	4.7	355	2	US-09-170-496D-130	Sequence 130, App
727	66	4.7	171	2	US-09-643-914-16	Sequence 16, Appl	800	65.5	4.7	355	2	US-09-170-496D-232	Sequence 232, App
728	66	4.7	171	2	US-09-742-361A-16	Sequence 16, Appl	801	65.5	4.7	355	2	US-09-917-254-68	Sequence 68, Appl
729	66	4.7	191	2	US-09-443-041A-24	Sequence 24, Appl	802	65.5	4.7	355	5	PCT-US93-11153-28	Sequence 28, Appl
730	66	4.7	216	2	US-10-224-880D-24	Sequence 24, Appl	803	65.5	4.7	355	5	PCT-US93-11153-32	Sequence 32, Appl
731	66	4.7	254	2	US-09-902-540-15766	Sequence 15766, A	804	65.5	4.7	356	2	US-09-107-532A-4245	Sequence 4245, Ap
732	66	4.7	260	2	US-09-443-041A-10	Sequence 10, Appl	805	65.5	4.7	391	2	US-09-107-532A-4209	Sequence 4209, Ap
733	66	4.7	260	2	US-10-224-880D-10	Sequence 10, Appl	806	65.5	4.7	391	2	US-09-543-681A-7029	Sequence 7029, Ap
734	66	4.7	281	2	US-09-134-001C-4763	Sequence 4763, Ap	807	65.5	4.7	391	2	US-09-248-796A-15698	Sequence 15698, A
735	66	4.7	345	2	US-09-252-991A-28113	Sequence 28113, A	808	65.5	4.7	393	2	US-09-351-150A-29	Sequence 29, Appl
736	66	4.7	355	1	US-08-846-762-93	Sequence 93, Appl	809	65.5	4.7	399	2	US-09-328-352-8043	Sequence 8043, Ap
737	66	4.7	357	2	US-09-303-518D-850	Sequence 850, App	810	65.5	4.7	399	2	US-09-560-761B-4	Sequence 4, Appli
738	66	4.7	367	2	US-09-134-001C-5557	Sequence 5557, Ap	811	65.5	4.7	422	2	US-09-809-665A-73	Sequence 73, Appl
739	66	4.7	393	2	US-09-134-001C-5594	Sequence 5594, Ap	812	65.5	4.7	426	7	5268463-8	Patent No. 5268463
740	66	4.7	400	2	US-09-198-452A-302	Sequence 302, App	813	65.5	4.7	427	2	US-09-438-185A-217	Sequence 217, App
741	66	4.7	400	2	US-09-438-185A-291	Sequence 291, App	814	65.5	4.7	428	1	US-08-570-157-5	Sequence 5, Appli
742	66	4.7	403	2	US-09-489-039A-11910	Sequence 11910, A	815	65.5	4.7	428	2	US-08-029-170-31	Sequence 31, Appl
743	66	4.7	415	2	US-09-080-044-6	Sequence 6, Appli	816	65.5	4.7	428	2	US-09-076-510-5	Sequence 5, Appli
744	66	4.7	415	2	US-09-531-857A-6	Sequence 6, Appli	817	65.5	4.7	428	2	US-09-004-349-5	Sequence 5, Appli
745	66	4.7	431	5	PCT-US91-00909-6	Sequence 6, Appli	818	65.5	4.7	428	2	US-09-443-745-31	Sequence 31, Appl
746	66	4.7	432	2	US-09-489-039A-7223	Sequence 7223, Ap	819	65.5	4.7	437	2	US-09-489-039A-8958	Sequence 8958, Ap
747	66	4.7	439	2	US-09-248-796A-20082	Sequence 20082, A	820	65.5	4.7	444	1	US-07-937-609-14	Sequence 14, Appl
748	66	4.7	464	2	US-09-252-991A-18525	Sequence 18525, A	821	65.5	4.7	444	2	US-08-029-170-14	Sequence 14, Appl
749	66	4.7	469	2	US-10-094-749-2536	Sequence 2536, Ap	822	65.5	4.7	444	2	US-09-443-745-14	Sequence 14, Appl
750	66	4.7	471	2	US-09-543-681A-5580	Sequence 5580, Ap	823	65.5	4.7	457	1	US-08-882-704A-6	Sequence 6, Appli
751	66	4.7	481	2	US-09-762-278-4	Sequence 4, Appli	824	65.5	4.7	457	2	US-09-151-957-6	Sequence 6, Appli
752	66	4.7	483	2	US-09-107-532A-4123	Sequence 4123, Ap	825	65.5	4.7	457	2	US-10-195-518-6	Sequence 6, Appli
753	66	4.7	486	2	US-09-489-039A-7706	Sequence 7706, Ap	826	65.5	4.7	465	2	US-09-328-352-5222	Sequence 5222, Ap
754	66	4.7	508	2	US-09-328-352-6467	Sequence 6467, Ap	827	65.5	4.7	490	2	US-09-252-991A-27210	Sequence 27210, A
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756	66	4.7	511	2	US-08-464-258B-8	Sequence 8, Appli	829	65.5	4.7	530	2	US-09-134-001C-4510	Sequence 4510, Ap

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831	65.5	4.7	600	2	US-09-438-185A-1013	Sequence 1013, Ap	904	65	4.7	518	2	US-09-548-373D-2	Sequence 2, Appli
832	65.5	4.7	601	1	US-07-676-174A-2	Sequence 2, Appli	905	65	4.7	518	2	US-09-795-847B-2	Sequence 2, Appli
833	65.5	4.7	697	2	US-09-603-208A-226	Sequence 226, App	906	65	4.7	518	2	US-09-869-414-2	Sequence 2, Appli
834	65.5	4.7	705	2	US-09-547-789-5	Sequence 5, Appli	907	65	4.7	518	2	US-09-548-366F-2	Sequence 2, Appli
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836	65.5	4.7	908	2	US-08-855-146-2	Sequence 2, Appli	909	65	4.7	518	2	US-09-794-925A-2	Sequence 2, Appli
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841	65.5	4.7	1036	2	US-09-560-876A-5	Sequence 5, Appli	914	65	4.7	518	2	US-09-794-743-2	Sequence 2, Appli
842	65.5	4.7	1065	2	US-09-560-876A-6	Sequence 6, Appli	915	65	4.7	518	2	US-09-999-833A-196	Sequence 196, App
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844	65	4.7	144	2	US-09-134-001C-3102	Sequence 3102, Ap	917	65	4.7	518	2	US-09-978-189-196	Sequence 196, App
845	65	4.7	154	2	US-09-955-732A-7	Sequence 7, Appli	918	65	4.7	518	2	US-10-017-085A-196	Sequence 196, App
846	65	4.7	168	2	US-09-544-716-15	Sequence 15, Appli	919	65	4.7	518	3	US-10-145-129A-196	Sequence 196, App
847	65	4.7	168	2	US-09-557-921-16	Sequence 16, Appli	920	65	4.7	518	3	US-10-013-929A-196	Sequence 196, App
848	65	4.7	168	2	US-09-564-357-18	Sequence 18, Appli	921	65	4.7	518	3	US-10-013-917A-196	Sequence 196, App
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851	65	4.7	168	2	US-09-527-376-12	Sequence 12, Appli	924	65	4.7	541	1	US-08-592-541-166	Sequence 166, App
852	65	4.7	168	2	US-09-775-925-27	Sequence 27, Appli	925	65	4.7	541	2	US-08-888-077A-21	Sequence 21, Appli
853	65	4.7	168	3	US-10-655-073-17	Sequence 17, Appli	926	65	4.7	541	2	US-09-124-698-166	Sequence 166, App
854	65	4.7	198	2	US-09-213-293D-9	Sequence 9, Appli	927	65	4.7	541	2	US-09-127-480-166	Sequence 166, App
855	65	4.7	202	2	US-09-107-433-3144	Sequence 3144, Ap	928	65	4.7	541	2	US-09-124-523-166	Sequence 166, App
856	65	4.7	274	2	US-09-489-039A-14140	Sequence 14140, A	929	65	4.7	541	2	US-09-636-796A-166	Sequence 166, App
857	65	4.7	306	2	US-09-248-796A-17619	Sequence 17619, A	930	65	4.7	541	2	US-09-949-016-11075	Sequence 11075, A
858	65	4.7	313	1	US-08-990-379-7	Sequence 7, Appli	931	65	4.7	545	2	US-09-198-452A-519	Sequence 519, App
859	65	4.7	314	2	US-09-164-193-22	Sequence 22, Appli	932	65	4.7	545	2	US-09-438-185A-483	Sequence 483, App
860	65	4.7	314	2	US-09-221-448A-22	Sequence 22, Appli	933	65	4.7	562	2	US-09-328-352-4694	Sequence 4694, Ap
861	65	4.7	315	2	US-09-393-634-56	Sequence 56, Appli	934	65	4.7	574	2	US-09-107-433-3877	Sequence 3877, Ap
862	65	4.7	318	2	US-09-270-767-45996	Sequence 45996, A	935	65	4.7	599	1	US-08-222-619-2	Sequence 2, Appli
863	65	4.7	331	2	US-09-252-991A-24546	Sequence 24546, A	936	65	4.7	599	2	US-08-221-767-24	Sequence 24, Appli
864	65	4.7	332	2	US-09-232-338-8	Sequence 8, Appli	937	65	4.7	599	5	PCT-US95-04075-2	Sequence 52, Appli
865	65	4.7	346	2	US-09-710-279-504	Sequence 504, App	938	65	4.7	617	2	US-10-154-419-52	Sequence 52, Appli
866	65	4.7	356	2	US-09-107-532A-6286	Sequence 6286, Ap	939	65	4.7	633	2	US-09-248-796A-20407	Sequence 20407, A
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868	65	4.7	367	2	US-09-252-991A-31459	Sequence 31459, A	941	65	4.7	738	2	US-09-107-532A-5096	Sequence 5096, Ap
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870	65	4.7	380	2	US-09-489-039A-8153	Sequence 8153, Ap	943	65	4.7	856	2	US-10-099-322-116	Sequence 116, App
871	65	4.7	383	2	US-09-710-279-2026	Sequence 2026, Ap	944	65	4.7	856	2	US-10-044-564-116	Sequence 116, App
872	65	4.7	387	2	US-09-710-279-3180	Sequence 3180, Ap	945	65	4.7	1095	2	US-09-636-215-780	Sequence 780, App
873	65	4.7	390	2	US-09-710-279-1422	Sequence 1422, Ap	946	65	4.7	1095	2	US-09-685-166A-780	Sequence 780, App
874	65	4.7	393	2	US-09-134-000C-4238	Sequence 4238, Ap	947	65	4.7	1095	2	US-09-679-426-780	Sequence 780, App
875	65	4.7	404	2	US-09-710-279-1204	Sequence 1204, Ap	948	65	4.7	1095	2	US-09-759-143-780	Sequence 780, App
876	65	4.7	405	2	US-09-543-681A-4311	Sequence 4311, Ap	949	65	4.7	1095	2	US-09-651-236-780	Sequence 780, App
877	65	4.7	406	2	US-09-134-001C-4084	Sequence 4084, Ap	950	65	4.7	1095	2	US-09-657-279-780	Sequence 780, App
878	65	4.7	415	2	US-09-134-001C-5101	Sequence 5101, Ap	951	65	4.7	1095	2	US-10-012-896-780	Sequence 780, App
879	65	4.7	423	2	US-09-824-551-2	Sequence 2, Appli	952	65	4.7	1095	3	US-10-144-678A-780	Sequence 780, App
880	65	4.7	426	2	US-09-252-991A-30025	Sequence 30025, A	953	65	4.7	1104	2	US-09-793-998-11	Sequence 11, Appli
881	65	4.7	433	2	US-09-949-016-8065	Sequence 8065, Ap	954	65	4.7	3174	1	US-08-477-451-3	Sequence 3, Appli
882	65	4.7	436	2	US-09-583-110-4729	Sequence 4729, Ap	955	64.5	4.6	157	2	US-09-605-703B-1500	Sequence 1500, Ap
883	65	4.7	440	2	US-09-107-433-5201	Sequence 5201, Ap	956	64.5	4.6	173	2	US-09-270-767-33313	Sequence 33313, A
884	65	4.7	446	2	US-09-134-000C-6454	Sequence 6454, Ap	957	64.5	4.6	173	2	US-09-270-767-48530	Sequence 48530, A
885	65	4.7	447	2	US-10-094-749-2670	Sequence 2670, Ap	958	64.5	4.6	238	2	US-09-134-001C-3136	Sequence 3136, Ap
886	65	4.7	447	2	US-09-489-039A-9027	Sequence 9027, Ap	959	64.5	4.6	240	2	US-09-543-681A-5483	Sequence 5483, Ap
887	65	4.7	459	2	US-09-489-039A-13479	Sequence 13479, A	960	64.5	4.6	256	2	US-10-104-047-2400	Sequence 2400, Ap
888	65	4.7	472	2	US-09-489-039A-13479	Sequence 13479, A	961	64.5	4.6	259	2	US-09-489-039A-11949	Sequence 11949, A
889	65	4.7	482	2	US-09-902-540-10594	Sequence 10594, A	962	64.5	4.6	260	2	US-08-983-075D-9	Sequence 9, Appli
890	65	4.7	490	2	US-09-134-001C-5116	Sequence 5116, Ap	963	64.5	4.6	263	2	US-09-949-016-10927	Sequence 10927, A
891	65	4.7	494	2	US-09-543-681A-7033	Sequence 7033, Ap	964	64.5	4.6	276	2	US-09-583-110-5031	Sequence 5031, Ap
892	65	4.7	503	2	US-09-134-001C-3096	Sequence 3096, Ap	965	64.5	4.6	284	2	US-09-107-433-3147	Sequence 3147, Ap
893	65	4.7	505	2	US-09-134-000C-5340	Sequence 5340, Ap	966	64.5	4.6	323	2	US-09-489-039A-7408	Sequence 7408, Ap
894	65	4.7	515	2	US-09-489-039A-12306	Sequence 12306, A	967	64.5	4.6	338	2	US-09-270-767-34974	Sequence 34974, A
895	65	4.7	518	2	US-08-999-723-2	Sequence 2, Appli	968	64.5	4.6	338	2	US-09-270-767-50191	Sequence 50191, A
896	65	4.7	518	2	US-09-434-427-2	Sequence 2, Appli	969	64.5	4.6	344	2	US-08-311-731A-172	Sequence 172, App
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898	65	4.7	518	2	US-09-548-367D-2	Sequence 2, Appli	971	64.5	4.6	398	2	US-09-348-930A-9	Sequence 9, Appli
899	65	4.7	518	2	US-09-551-853D-2	Sequence 2, Appli	972	64.5	4.6	398	2	US-09-578-063-75	Sequence 75, Appli
900	65	4.7	518	2	US-09-215-450-19	Sequence 19, Appli	973	64.5	4.6	398	3	US-09-333-159-75	Sequence 75, Appli
901	65	4.7	518	2	US-09-416-901B-2	Sequence 2, Appli	974	64.5	4.6	399	2	US-09-328-352-7394	Sequence 7394, Ap
902	65	4.7	518	2	US-09-548-376D-2	Sequence 2, Appli	975	64.5	4.6	404	2	US-09-489-039A-8947	Sequence 8947, Ap

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977	64.5	4.6	411	2	US-09-527-431-80	Sequence 80, Appl	1050	64	4.6	389	1	US-08-846-705-2	Sequence 2, Appli
978	64.5	4.6	411	2	US-09-446-861-80	Sequence 80, Appl	1051	64	4.6	389	2	US-09-211-823C-23	Sequence 23, Appl
979	64.5	4.6	412	2	US-09-198-452A-901	Sequence 901, App	1052	64	4.6	394	2	US-09-710-279-3292	Sequence 3292, Ap
980	64.5	4.6	413	2	US-09-438-185A-838	Sequence 838, App	1053	64	4.6	398	2	US-09-489-039A-13159	Sequence 13159, A
981	64.5	4.6	416	2	US-09-540-236-2393	Sequence 2393, Ap	1054	64	4.6	402	2	US-08-846-704-4	Sequence 4, Appli
982	64.5	4.6	431	2	US-09-900-237-28	Sequence 28, Appl	1055	64	4.6	402	2	US-08-462-509B-2	Sequence 2, Appli
983	64.5	4.6	436	2	US-09-949-016-11448	Sequence 11448, A	1056	64	4.6	402	5	PCT-US95-05616-2	Sequence 2, Appli
984	64.5	4.6	439	2	US-09-710-279-2408	Sequence 2408, Ap	1057	64	4.6	415	2	US-09-134-000C-4092	Sequence 4092, Ap
985	64.5	4.6	459	2	US-09-134-001C-4856	Sequence 4856, Ap	1058	64	4.6	425	2	US-08-846-704-2	Sequence 2, Appli
986	64.5	4.6	462	2	US-09-902-540-10036	Sequence 10036, A	1059	64	4.6	425	2	US-09-479-128-2	Sequence 2, Appli
987	64.5	4.6	470	1	US-08-724-394A-10	Sequence 10, Appl	1060	64	4.6	425	2	US-09-211-823C-22	Sequence 22, Appl
988	64.5	4.6	493	2	US-09-489-039A-13709	Sequence 13709, A	1061	64	4.6	425	2	US-09-826-509-549	Sequence 549, App
989	64.5	4.6	517	2	US-09-815-923-16	Sequence 16, Appl	1062	64	4.6	428	2	US-09-345-236B-62	Sequence 62, Appl
990	64.5	4.6	534	2	US-09-252-991A-31719	Sequence 31719, A	1063	64	4.6	430	1	US-08-601-435-2	Sequence 2, Appli
991	64.5	4.6	539	2	US-09-518-959-8	Sequence 8, Appli	1064	64	4.6	430	1	US-08-931-047-2	Sequence 2, Appli
992	64.5	4.6	539	2	US-09-518-959-9	Sequence 9, Appli	1065	64	4.6	430	1	US-08-783-202-2	Sequence 2, Appli
993	64.5	4.6	549	2	US-09-115-150-4	Sequence 4, Appli	1066	64	4.6	430	1	US-08-443-041A-31	Sequence 31, Appl
994	64.5	4.6	549	2	US-09-489-039A-8237	Sequence 8237, Ap	1067	64	4.6	430	2	US-10-224-880D-31	Sequence 31, Appl
995	64.5	4.6	550	2	US-09-721-870-18	Sequence 18, Appl	1068	64	4.6	441	2	US-09-593-110-4400	Sequence 4400, Ap
996	64.5	4.6	555	2	US-09-543-681A-4582	Sequence 4582, Ap	1069	64	4.6	445	2	US-09-107-433-5039	Sequence 5039, Ap
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1001	64.5	4.6	672	1	US-07-841-651-3	Sequence 3, Appli	1074	64	4.6	470	2	US-10-094-749-2224	Sequence 2224, Ap
1002	64.5	4.6	674	2	US-09-540-236-3546	Sequence 3546, Ap	1075	64	4.6	476	2	US-09-134-001C-3778	Sequence 3778, Ap
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1004	64.5	4.6	723	2	US-09-248-796A-15245	Sequence 15245, A	1077	64	4.6	495	2	US-09-915-181A-7	Sequence 7, Appli
1005	64.5	4.6	723	3	US-10-114-270-144	Sequence 144, App	1078	64	4.6	501	2	US-09-328-352-6371	Sequence 6371, Ap
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1010	64.5	4.6	908	1	US-07-903-456-2	Sequence 2, Appli	1083	64	4.6	543	2	US-09-605-703B-1198	Sequence 1198, Ap
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1013	64.5	4.6	908	2	US-09-949-016-7025	Sequence 7025, Ap	1086	64	4.6	613	2	US-09-107-532A-6935	Sequence 6935, Ap
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1018	64	4.6	125	2	US-09-270-767-51697	Sequence 51697, A	1091	64	4.6	816	2	US-09-248-796A-20939	Sequence 20939, A
1019	64	4.6	135	2	US-09-270-767-32080	Sequence 32080, A	1092	64	4.6	823	2	US-09-949-016-6852	Sequence 6852, Ap
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1022	64	4.6	205	2	US-09-540-236-2955	Sequence 2955, Ap	1095	64	4.6	1042	2	US-09-512-250C-32	Sequence 32, Appl
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1024	64	4.6	238	2	US-09-903-190-89	Sequence 89, Appl	1097	64	4.6	1094	2	US-09-712-363-287	Sequence 287, App
1025	64	4.6	250	2	US-09-543-681A-4487	Sequence 4487, Ap	1098	64	4.6	1278	2	US-09-462-136-2	Sequence 2, Appli
1026	64	4.6	258	2	US-09-328-352-4425	Sequence 4425, Ap	1099	64	4.6	1318	2	US-09-949-016-10152	Sequence 10152, A
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1028	64	4.6	296	2	US-09-724-623-103	Sequence 103, App	1101	64	4.6	1551	2	US-10-418-036-12	Sequence 12, Appl
1029	64	4.6	296	3	US-10-288-930-103	Sequence 195, App	1102	63.5	4.6	175	2	US-08-858-207A-363	Sequence 363, App
1030	64	4.6	303	3	US-10-770-127-195	Sequence 33, Appl	1103	63.5	4.6	221	2	US-09-248-796A-16290	Sequence 16290, A
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1127	63.5	4.6	341	2	US-10-094-749-2185	Sequence 2185, Ap	1200	63	4.5	259	2	US-09-328-352-6237	Sequence 6237, Ap
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1129	63.5	4.6	356	2	US-08-567-882-7	Sequence 7, Appli	1202	63	4.5	273	2	US-09-949-016-8333	Sequence 8333, Ap
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1132	63.5	4.6	379	1	US-08-227-108-18	Sequence 18, Appl	1205	63	4.5	284	2	US-09-270-767-48852	Sequence 48852, A
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1135	63.5	4.6	404	1	US-08-428-243-7	Sequence 7, Appli	1208	63	4.5	290	2	US-09-910-174B-8	Sequence 8, Appli
1136	63.5	4.6	404	5	PCT-US93-10301-7	Sequence 7, Appli	1209	63	4.5	290	2	US-09-620-461-8	Sequence 8, Appli
1137	63.5	4.6	405	2	US-09-248-796A-17965	Sequence 17965, A	1210	63	4.5	290	2	US-09-451-291-1	Sequence 1, Appli
1138	63.5	4.6	414	2	US-09-489-039A-10869	Sequence 10869, A	1211	63	4.5	290	2	US-09-645-069-4	Sequence 4, Appli
1139	63.5	4.6	430	2	US-09-583-110-4230	Sequence 4230, Ap	1212	63	4.5	290	2	US-09-915-789A-17	Sequence 17, Appl
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1145	63.5	4.6	470	2	US-09-543-681A-4625	Sequence 4625, Ap	1218	63	4.5	345	2	US-09-107-532A-4426	Sequence 4426, Ap
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1148	63.5	4.6	473	2	US-08-879-337-7	Sequence 7, Appli	1221	63	4.5	345	2	US-09-997-333-2	Sequence 2, Appli
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1153	63.5	4.6	488	1	US-08-586-897-2	Sequence 2, Appli	1226	63	4.5	345	3	US-09-989-728-2	Sequence 2, Appli
1154	63.5	4.6	488	2	US-09-826-509-561	Sequence 561, App	1227	63	4.5	345	3	US-09-997-349-2	Sequence 2, Appli
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1156	63.5	4.6	531	2	US-09-489-039A-9781	Sequence 9781, Ap	1229	63	4.5	345	3	US-09-989-293A-2	Sequence 2, Appli
1157	63.5	4.6	534	2	US-09-710-279-920	Sequence 920, App	1230	63	4.5	346	2	US-09-149-476-493	Sequence 493, App
1158	63.5	4.6	542	2	US-09-830-123-2	Sequence 2, Appli	1231	63	4.5	350	2	US-09-902-540-14418	Sequence 14418, A
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1164	63.5	4.6	652	2	US-08-956-322-2	Sequence 2, Appli	1237	63	4.5	374	2	US-09-721-341-8	Sequence 8, Appli
1165	63.5	4.6	658	2	US-09-492-709A-352	Sequence 352, App	1238	63	4.5	374	2	US-09-721-495B-8	Sequence 8, Appli
1166	63.5	4.6	658	2	US-09-538-092-1190	Sequence 1190, Ap	1239	63	4.5	374	2	US-09-721-341-8	Sequence 8, Appli
1167	63.5	4.6	685	2	US-09-720-317A-31	Sequence 31, Appl	1240	63	4.5	387	2	US-09-549-848B-17	Sequence 17, Appl
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1172	63.5	4.6	799	2	US-10-104-047-2335	Sequence 2335, Ap	1245	63	4.5	409	2	US-09-605-703B-2146	Sequence 2146, Ap
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1174	63.5	4.6	850	2	US-09-583-110-4394	Sequence 4394, Ap	1247	63	4.5	424	2	US-09-543-681A-4762	Sequence 4762, Ap
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1178	63.5	4.6	977	2	US-10-104-047-2552	Sequence 2552, Ap	1251	63	4.5	430	2	US-10-224-880D-18	Sequence 18, Appl
1179	63.5	4.6	1007	2	US-10-209-059-28	Sequence 28, Appl	1252	63	4.5	438	1	US-08-677-049-9	Sequence 9, Appli
1180	63.5	4.6	1065	2	US-09-221-013A-10	Sequence 10, Appl	1253	63	4.5	443	1	US-08-570-157-6	Sequence 6, Appli
1181	63.5	4.6	1098	2	US-08-726-214-10	Sequence 10, Appl	1254	63	4.5	443	2	US-09-076-510-6	Sequence 6, Appli
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1183	63.5	4.6	1895	2	US-09-487-558B-136	Sequence 136, App	1256	63	4.5	454	2	US-09-830-230A-33	Sequence 33, Appl
1184	63.5	4.6	2522	2	US-09-251-645-13	Sequence 13, Appl	1257	63	4.5	461	1	US-08-194-338-4	Sequence 4, Appli
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1186	63	4.5	143	2	US-09-107-433-4477	Sequence 4477, Ap	1259	63	4.5	478	2	US-09-107-532A-6105	Sequence 6105, Ap
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1191	63	4.5	219	1	US-08-640-386A-4	Sequence 4, Appli	1264	63	4.5	521	2	US-09-134-001C-4290	Sequence 4290, Ap
1192	63	4.5	249	2	US-09-902-540-13089	Sequence 13089, Ap	1265	63	4.5	554	2	US-09-540-236-2634	Sequence 2634, Ap
1193	63	4.5	250	2	US-09-107-532A-6270	Sequence 6270, Ap	1266	63	4.5	580	2	US-09-657-252-2	Sequence 2, Appli
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ALIGNMENTS

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; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
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QY      121  HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLLVIWCGVSALSMLTCSSVL 180
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Db      121  HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLLVIWCGVSALSMLTCSSVL 180

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RESULT 2
US-09-990-444-23
; Sequence 23, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-144;  
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QY 181 HSGNFGTDLEQKHLWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEAN 240  
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QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266  
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RESULT 4  
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; Sequence 23, Application US/09992598  
; Patent No. 6956108  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
  
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Best Local Similarity 100.0%; Pred. No. 1.2e-144;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 5  
US-09-989-735-23  
; Sequence 23, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
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; CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1998-06-24





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RESULT 7
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; Sequence 23, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 23, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/091982
;	PRIOR FILING DATE:	1998-07-07
;	PRIOR APPLICATION NUMBER:	60/092182
;	PRIOR FILING DATE:	1998-07-09

Query Match	100.0%;	Score 1392;	DB 3;	Length 266;
Best Local Similarity	100.0%;	Pred. No. 1.2e-144;		
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db	1	MMWFOQGLSFLPSALVIWTSAAFI <th>FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML</th> <th>60</th>	FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60

Qy	61	NIAAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVGLISCLGLSIVANFQKTTLF	120
Dd	61	NIAAVLCIATIIYVRYKQVHALSPEENVIIKLNKAGLVGLISCLGLSIVANFQKTTLF	120
Qy	121	HVSGAVLTFMGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMITCSSL	180
Dd	121	HVSGAVLTFMGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMITCSSL	180
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## RESULT 9

US-09-997-349-23

; Sequence 23, Application US/09997349

; Patent No. 7034106

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

; FILE REFERENCE: P2730P1C37

; CURRENT APPLICATION NUMBER: US/09/997,349

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MWMFQQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
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Db 1 MWMFQQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
61 NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120
|||||
Db 61 NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120
121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIMCGVSALSMLTCSSVL 180
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Db 121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIMCGVSALSMLTCSSVL 180
181 HSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240
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241 LHGLTLYDTAPCPINNERTLLSRDI 266
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RESULT 10
US-09-997-653-23
; Sequence 23, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25



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; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
   |||||||
Db 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120
   |||||||
Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

QY 121 HVSGAVLTFMGSLYMFVQTIISYQMPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVL 180
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Db 121 HVSGAVLTFMGSLYMFVQTIISYQMPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVL 180

QY 181 HSGNFGTDLEQKLNHNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFQKISLRVEAN 240
   |||||||
Db 181 HSGNFGTDLEQKLNHNWPNEDKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFQKISLRVEAN 240

QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
   |||||||
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266

RESULT 11
US-09-989-293A-23
; Sequence 23, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: 60/089512  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089514  
; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR APPLICATION NUMBER: 60/090862  
; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/090863

; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
  
Query Match 100.0%; Score 1392; DB 3; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-144;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MWWFQQLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
Db 1 MWWFQQLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
  
Qy 61 NIAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120  
Db 61 NIAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120  
  
Qy 121 HVSGAVLTFGMSLYMFVQITLSYQMPKIHGKQVFWIRLLLVWCGVSALSLTCSVL 180  
Db 121 HVSGAVLTFGMSLYMFVQITLSYQMPKIHGKQVFWIRLLLVWCGVSALSLTCSVL 180  
  
Qy 181 HSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
Db 181 HSGNFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFSFFGFFLTYYIRDFQKISLRVEAN 240  
  
Qy 241 LHGLTLYDTAPCPINNERLRLSRDI 266  
Db 241 LHGLTLYDTAPCPINNERLRLSRDI 266  
  
RESULT 12  
US-09-663-600A-190  
; Sequence 190, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31.US3.CIP  
; CURRENT APPLICATION NUMBER: US/09/663,600A  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm



SEQ ID NO 190  
LENGTH: 267  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -21...-1  
US-09-663-600A-190

Query Match 99.7%; Score 1388; DB 2; Length 267;  
Best Local Similarity 99.6%; Pred. No. 3.2e-144;  
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MWVFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
Db 1 MWVFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

Qy 121 HVSGAVLTFGMSLYMFVQTIISYQMPKIHKQVFWIRLLLVICGVSALSMLTCSVL 180  
Db 121 HVSGAVLTFGMSLYMFVQTIISYQMPKIHKQVFWIRLLLVICGVSALSMLTCSVL 180

Qy 181 HSGNFGTDLEQKLNHPEDKGYVLMHTTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
Db 181 HSGNFGTDLEQKLNHPEDKGYVLMHTTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240

Qy 241 LHGLTYDTAPCPINNERLLSRDI 266  
Db 241 LHGLTYDTAPCPINNERLLSRDI 266

RESULT 13  
US-09-663-600A-96

Sequence 96, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/099,273  
PRIOR FILING DATE: 1998-09-04  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: Patent.pm  
SEQ ID NO 96  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -21...-1  
US-09-663-600A-96

Query Match 42.8%; Score 595.5; DB 2; Length 172;  
Best Local Similarity 79.4%; Pred. No. 2.4e-57;

Matches 123; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Qy 1 MWVFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
Db 1 MWVFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQENPFCC 120

Qy 121 HV--SGAVLTFGMSLYMFVQTIISYQMPKIHK 153  
Db 121 TCKWSCAYLWYGL-IYVCSDPFLPKCSPKSNKG 154

RESULT 14  
US-09-724-864-38

Sequence 38, Application US/09724864  
Patent No. 6380362  
GENERAL INFORMATION:  
APPLICANT: Watson, James D  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
TITLE OF INVENTION: by the polynucleotides and methods for their use.  
FILE REFERENCE: 11000.105001  
CURRENT APPLICATION NUMBER: US/09/724,864  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 238  
TYPE: PRT  
ORGANISM: Mouse  
US-09-724-864-38

Query Match 34.4%; Score 479.5; DB 2; Length 238;  
Best Local Similarity 37.3%; Pred. No. 2.2e-44;  
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

Qy 1 MWVFQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
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Db 61 NFSAPLGAATMYTRYKIVEKQNETCYFSTPVFNLV-----SLALGLVCIGMIVANFQ 114

Qy 114 KTTLFAAHVSGAVLTFGMSLYMFVQTIISYQMPKIHKQVFWIRLLLVICGVSALS 173  
Db 115 ELAVPVVDGALLAFVCGVVYTLQLSIYSYKSCPQWNSLTTCVNRMAISAVCAA 174

Qy 174 LTCSSVLHSGNFGTDLEQKLNHPEDKGYVLMHTTAAEWSMSFSFFGFFLTYYIRDFQKI 233  
Db 175 IACASLISI-----TKLEWNPKEKDYIYHVVSACEWTVAFGFIFYELTFIQDFQSV 226

Qy 234 SLRVEANLH 242  
Db 227 TLRISTEIN 235

RESULT 15  
US-09-663-600A-130

Sequence 130, Application US/09663600A  
Patent No. 6573068  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
FILE REFERENCE: 31.US3.CIP  
CURRENT APPLICATION NUMBER: US/09/663,600A

Search completed: August 28, 2006, 17:43:02  
Job time : 69 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
  
OM protein - protein search, using sw model  
  
Run on: August 28, 2006, 17:37:50 ; Search time 34 Seconds  
(without alignments)  
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Perfect score: 1392  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
  
Searched: 247503 seqs, 68422524 residues  
  
Total number of hits satisfying chosen parameters: 247503  
  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1392	100.0	266	US-10-196-749-10	Sequence 10, Appl
2	1392	100.0	266	US-11-101-316-2	Sequence 2, Appl
3	1392	100.0	266	US-11-376-673-2	Sequence 2, Appl
4	486.5	34.9	238	US-11-293-697-2867	Sequence 2867, Ap
5	151.5	10.9	437	US-11-395-249-66	Sequence 66, Appl
6	99	7.1	187	US-11-293-697-4787	Sequence 4787, Ap
7	93.5	6.7	303	US-11-056-355B-83608	Sequence 83608, A
8	93.5	6.7	379	US-11-056-355B-83607	Sequence 83607, A
9	88	6.3	312	US-11-056-355B-4953	Sequence 4953, Ap
10	88	6.3	313	US-11-056-355B-4952	Sequence 4952, Ap
11	88	6.3	932	US-10-449-902-35289	Sequence 35289, A
12	88	6.3	932	US-10-449-902-55200	Sequence 55200, A
13	87.5	6.3	482	US-11-330-403-16766	Sequence 16766, A
14	86	6.2	372	US-10-471-571A-4918	Sequence 4918, Ap
15	85.5	6.1	481	US-11-178-538-37	Sequence 37, Appl
16	85.5	6.1	545	US-11-395-249-26	Sequence 26, Appl
17	85	6.1	453	US-10-449-902-47037	Sequence 47037, A
18	84.5	6.1	271	US-11-056-355B-8562	Sequence 8562, Ap
19	84.5	6.1	278	US-11-056-355B-8561	Sequence 8561, Ap
20	84.5	6.1	288	US-11-056-355B-8560	Sequence 8560, Ap
21	84.5	6.1	370	US-11-174-307B-4896	Sequence 4896, Ap
22	84.5	6.1	453	US-10-196-749-84	Sequence 84, Appl
23	84.5	6.1	479	US-10-449-902-40971	Sequence 40971, A
24	84.5	6.1	515	US-11-330-403-1950	Sequence 1950, Ap
25	83.5	6.0	468	US-11-330-403-18369	Sequence 18369, A

26	83.5	6.0	618	7	US-11-178-538-2	Sequence 2, Appl
27	83	6.0	250	7	US-11-056-355B-83609	Sequence 83609, A
28	82	5.9	219	6	US-10-539-228-480	Sequence 480, App
29	82	5.9	319	7	US-11-056-355B-42784	Sequence 42784, A
30	82	5.9	356	7	US-11-056-355B-42783	Sequence 42783, A
31	82	5.9	376	7	US-11-056-355B-42782	Sequence 42782, A
32	82	5.9	488	7	US-11-056-355B-91797	Sequence 91797, A
33	82	5.9	488	7	US-11-056-355B-95553	Sequence 95553, A
34	82	5.9	488	7	US-11-330-403-16425	Sequence 16425, A
35	81.5	5.9	294	7	US-11-056-355B-62351	Sequence 62351, A
36	81.5	5.9	334	7	US-11-056-355B-62350	Sequence 62350, A
37	81	5.8	234	7	US-11-347-766-34	Sequence 34, Appl
38	81	5.8	342	6	US-10-449-902-32686	Sequence 32686, A
39	81	5.8	422	6	US-10-449-902-32842	Sequence 32842, A
40	81	5.8	422	6	US-10-449-902-53486	Sequence 53486, A
41	81	5.8	422	6	US-10-449-902-53550	Sequence 53550, A
42	81	5.8	487	7	US-11-330-403-7405	Sequence 7405, Ap
43	80.5	5.8	359	6	US-10-471-571A-3590	Sequence 3590, Ap
44	80.5	5.8	473	7	US-11-330-403-15463	Sequence 15463, A
45	80	5.7	516	6	US-10-449-902-40874	Sequence 40874, A
46	80	5.7	516	7	US-11-296-657-5	Sequence 5, Appl
47	79.5	5.7	596	6	US-10-449-902-34689	Sequence 34689, A
48	79.5	5.7	697	6	US-10-449-902-49799	Sequence 49799, A
49	79	5.7	250	7	US-11-330-403-5089	Sequence 5089, Ap
50	79	5.7	289	7	US-11-330-403-4684	Sequence 4684, Ap
51	79	5.7	363	7	US-11-056-355B-102923	Sequence 102923, A
52	79	5.7	363	7	US-11-056-355B-114162	Sequence 114162, A
53	79	5.7	373	7	US-11-056-355B-102922	Sequence 102922, A
54	79	5.7	373	7	US-11-056-355B-114161	Sequence 114161, A
55	79	5.7	377	7	US-11-056-355B-102921	Sequence 102921, A
56	79	5.7	377	7	US-11-056-355B-114160	Sequence 114160, A
57	79	5.7	468	6	US-10-449-902-47531	Sequence 47531, A
58	78.5	5.6	288	6	US-10-449-902-28626	Sequence 28626, A
59	78.5	5.6	288	6	US-10-449-902-32821	Sequence 32821, A
60	78.5	5.6	288	6	US-10-449-902-42640	Sequence 42640, A
61	78.5	5.6	288	6	US-10-449-902-43067	Sequence 43067, A
62	78.5	5.6	424	7	US-11-056-355B-17925	Sequence 17925, A
63	78.5	5.6	428	7	US-11-056-355B-17924	Sequence 17924, A
64	78.5	5.6	461	7	US-11-056-355B-88784	Sequence 88784, A
65	78.5	5.6	461	7	US-11-056-355B-92540	Sequence 92540, A
66	78.5	5.6	468	7	US-11-056-355B-88783	Sequence 88783, A
67	78.5	5.6	468	7	US-11-056-355B-92539	Sequence 92539, A
68	78.5	5.6	470	7	US-11-330-403-9708	Sequence 9708, Ap
69	78.5	5.6	479	7	US-11-056-355B-17923	Sequence 17923, A
70	78.5	5.6	498	7	US-11-056-355B-88782	Sequence 88782, A
71	78.5	5.6	498	7	US-11-056-355B-92538	Sequence 92538, A
72	78.5	5.6	624	7	US-11-056-355B-77797	Sequence 77797, A
73	78.5	5.6	630	7	US-11-056-355B-77796	Sequence 77796, A
74	78.5	5.6	793	7	US-11-325-276-18	Sequence 18, Appl
75	78	5.6	233	7	US-11-367-182-15	Sequence 15, Appl
76	78	5.6	309	7	US-11-178-538-55	Sequence 55, Appl
77	78	5.6	309	7	US-11-178-538-62	Sequence 62, Appl
78	78	5.6	349	6	US-10-953-349-14110	Sequence 14110, A
79	78	5.6	349	7	US-11-056-355B-59893	Sequence 59893, A
80	78	5.6	355	6	US-10-953-349-14109	Sequence 14109, A
81	78	5.6	355	7	US-11-056-355B-59892	Sequence 59892, A
82	78	5.6	362	6	US-10-953-349-14108	Sequence 14108, A
83	78	5.6	362	7	US-11-056-355B-59891	Sequence 59891, A
84	77.5	5.6	288	7	US-11-330-403-9006	Sequence 9006, Ap
85	77.5	5.6	316	6	US-10-449-902-55240	Sequence 55240, A
86	77.5	5.6	392	7	US-11-056-355B-41822	Sequence 41822, A
87	77.5	5.6	392	7	US-11-056-355B-44866	Sequence 44866, A
88	77.5	5.6	394	7	US-11-056-355B-41821	Sequence 41821, A
89	77.5	5.6	396	6	US-10-449-902-51643	Sequence 51643, A
90	77.5	5.6	445	7	US-11-056-355B-44865	Sequence 44865, A
91	77.5	5.6	473	7	US-11-056-355B-70692	Sequence 70692, A
92	77.5	5.6	480	7	US-11-056-355B-70691	Sequence 70691, A
93	77.5	5.6	491	7	US-11-056-355B-80245	Sequence 80245, A
94	77.5	5.6	498	7	US-11-056-355B-80244	Sequence 80244, A
95	77.5	5.6	510	7	US-11-056-355B-70690	Sequence 70690, A
96	77.5	5.6	526	7	US-11-056-355B-80243	Sequence 80243, A
97	77.5	5.6	635	7	US-11-056-355B-44864	Sequence 44864, A
98	77	5.5	313	6	US-10-449-902-49599	Sequence 49599, A

99	77	5.5	354	6	US-10-449-902-43952	Sequence 43952, A	172	72.5	5.2	456	7	US-11-330-403-429	Sequence 429, App
100	77	5.5	416	7	US-11-330-403-9143	Sequence 9143, Ap	173	72.5	5.2	461	7	US-11-056-355B-70764	Sequence 70764, A
101	76.5	5.5	211	7	US-11-056-355B-46703	Sequence 46703, A	174	72.5	5.2	461	7	US-11-330-403-12512	Sequence 12512, A
102	76.5	5.5	211	7	US-11-056-355B-47370	Sequence 47370, A	175	72.5	5.2	525	6	US-10-449-902-43268	Sequence 43268, A
103	76.5	5.5	634	6	US-10-449-902-44817	Sequence 44817, A	176	72.5	5.2	525	6	US-10-449-902-50345	Sequence 50345, A
104	76	5.5	236	7	US-11-056-355B-4954	Sequence 4954, Ap	177	72.5	5.2	688	7	US-11-330-403-11383	Sequence 11383, A
105	76	5.5	287	7	US-11-330-403-3241	Sequence 3241, Ap	178	72	5.2	337	7	US-11-347-870-20	Sequence 20, Appl
106	75.5	5.4	228	7	US-11-056-355B-73049	Sequence 73049, A	179	72	5.2	337	7	US-11-296-615-20	Sequence 20, Appl
107	75.5	5.4	282	7	US-11-056-355B-73048	Sequence 73048, A	180	72	5.2	338	7	US-11-204-427-3	Sequence 3, Appli
108	75.5	5.4	439	7	US-11-342-731-4	Sequence 4, Appli	181	72	5.2	344	7	US-11-056-355B-17517	Sequence 17517, A
109	75.5	5.4	476	7	US-11-056-355B-12403	Sequence 5398, Ap	182	72	5.2	423	7	US-11-056-355B-17516	Sequence 17516, A
110	75.5	5.4	500	7	US-11-024-544A-172	Sequence 12403, A	183	72	5.2	440	7	US-11-056-355B-91630	Sequence 91630, A
111	75.5	5.4	500	7	US-11-190-750-140	Sequence 172, App	184	72	5.2	440	7	US-11-056-355B-95386	Sequence 95386, A
112	75.5	5.4	500	7	US-11-056-355B-12402	Sequence 140, App	185	72	5.2	442	7	US-11-056-355B-17515	Sequence 17515, A
113	75.5	5.4	530	7	US-11-056-355B-12401	Sequence 12402, A	186	72	5.2	460	6	US-10-449-902-56742	Sequence 56742, A
114	75.5	5.4	545	7	US-11-056-355B-12401	Sequence 12401, A	187	72	5.2	464	7	US-11-330-403-17886	Sequence 17886, A
115	75	5.4	249	7	US-11-056-355B-22220	Sequence 22220, A	188	72	5.2	542	6	US-10-449-902-33358	Sequence 33358, A
116	75	5.4	254	7	US-11-056-355B-22219	Sequence 22219, A	189	72	5.2	542	6	US-10-449-902-42805	Sequence 42805, A
117	75	5.4	258	6	US-10-449-902-42650	Sequence 42650, A	190	72	5.2	542	6	US-10-449-902-43047	Sequence 43047, A
118	74.5	5.4	327	7	US-11-056-355B-102309	Sequence 102309, A	191	72	5.2	542	6	US-10-449-902-51839	Sequence 51839, A
119	74.5	5.4	327	7	US-11-056-355B-113548	Sequence 113548, A	192	72	5.2	582	7	US-11-056-355B-80100	Sequence 80100, A
120	74.5	5.4	339	6	US-10-449-902-56532	Sequence 56532, A	193	71.5	5.1	254	7	US-11-330-403-17896	Sequence 17896, A
121	74.5	5.4	345	7	US-11-056-355B-41823	Sequence 41823, A	194	71.5	5.1	260	6	US-10-471-571A-4750	Sequence 4750, Ap
122	74.5	5.4	347	7	US-11-056-355B-102308	Sequence 102308, A	195	71.5	5.1	363	7	US-11-056-355B-42530	Sequence 42530, A
123	74.5	5.4	347	7	US-11-056-355B-113547	Sequence 113547, A	196	71.5	5.1	382	7	US-11-056-355B-42529	Sequence 42529, A
124	74.5	5.4	411	7	US-11-330-403-7942	Sequence 7942, Ap	197	71.5	5.1	393	7	US-11-056-355B-42528	Sequence 42528, A
125	74.5	5.4	461	7	US-11-056-355B-91798	Sequence 91798, A	198	71.5	5.1	412	6	US-10-471-571A-2744	Sequence 2744, Ap
126	74.5	5.4	461	7	US-11-056-355B-95554	Sequence 95554, A	199	71.5	5.1	460	6	US-10-449-902-48146	Sequence 48146, A
127	74.5	5.4	535	6	US-10-449-902-51331	Sequence 51331, A	200	71.5	5.1	501	6	US-10-449-902-46591	Sequence 46591, A
128	74	5.3	382	6	US-10-449-902-50854	Sequence 50854, A	201	71.5	5.1	504	7	US-11-197-712-379	Sequence 379, App
129	74	5.3	383	6	US-10-953-349-5125	Sequence 5125, Ap	202	71.5	5.1	603	7	US-11-056-355B-50526	Sequence 50526, A
130	74	5.3	385	6	US-10-449-902-49336	Sequence 49336, A	203	71.5	5.1	665	7	US-11-056-355B-50525	Sequence 50525, A
131	74	5.3	404	7	US-11-330-403-4592	Sequence 4592, Ap	204	71.5	5.1	1053	6	US-10-449-902-41514	Sequence 41514, A
132	74	5.3	409	6	US-10-953-349-5124	Sequence 5124, Ap	205	71	5.1	261	6	US-10-196-749-356	Sequence 356, App
133	74	5.3	532	6	US-10-953-349-5123	Sequence 5123, Ap	206	71	5.1	261	7	US-11-101-316-118	Sequence 118, App
134	74	5.3	979	6	US-10-449-902-41275	Sequence 41275, A	207	71	5.1	261	7	US-11-376-673-118	Sequence 118, App
135	73.5	5.3	337	7	US-11-178-538-38	Sequence 38, Appl	208	71	5.1	405	6	US-10-449-902-43622	Sequence 43622, A
136	73.5	5.3	366	7	US-11-056-355B-88357	Sequence 88357, A	209	71	5.1	438	7	US-11-330-403-2109	Sequence 2109, Ap
137	73.5	5.3	366	7	US-11-056-355B-92113	Sequence 92113, A	210	71	5.1	448	7	US-11-330-403-16813	Sequence 16813, A
138	73.5	5.3	370	7	US-11-056-355B-88356	Sequence 88356, A	211	71	5.1	456	7	US-11-056-355B-89701	Sequence 89701, A
139	73.5	5.3	370	7	US-11-056-355B-92112	Sequence 92112, A	212	71	5.1	456	7	US-11-056-355B-93457	Sequence 93457, A
140	73.5	5.3	384	7	US-11-056-355B-88355	Sequence 88355, A	213	71	5.1	457	6	US-10-449-902-51106	Sequence 51106, A
141	73.5	5.3	384	7	US-11-056-355B-92111	Sequence 92111, A	214	71	5.1	457	7	US-11-056-355B-6882	Sequence 6882, Ap
142	73.5	5.3	441	7	US-11-330-403-18115	Sequence 92111, A	215	71	5.1	466	6	US-10-471-571A-5276	Sequence 5276, Ap
143	73.5	5.3	494	7	US-11-056-355B-91629	Sequence 18115, A	216	71	5.1	467	7	US-11-330-403-14572	Sequence 14572, A
144	73.5	5.3	494	7	US-11-056-355B-95385	Sequence 91629, A	217	71	5.1	487	6	US-10-449-902-37219	Sequence 37219, A
145	73.5	5.3	498	6	US-10-471-571A-192	Sequence 95385, A	218	71	5.1	488	7	US-11-056-355B-6881	Sequence 6881, Ap
146	73.5	5.3	522	7	US-11-056-355B-91628	Sequence 192, App	219	71	5.1	502	6	US-10-545-334-2	Sequence 2, Appli
147	73.5	5.3	522	7	US-11-056-355B-95384	Sequence 91628, A	220	71	5.1	506	7	US-11-056-355B-89700	Sequence 89700, A
148	73.5	5.3	811	6	US-10-449-902-44848	Sequence 95384, A	221	71	5.1	506	7	US-11-056-355B-93456	Sequence 93456, A
149	73.5	5.3	1080	7	US-11-056-355B-69790	Sequence 44848, A	222	71	5.1	510	7	US-11-056-355B-6880	Sequence 6880, Ap
150	73.5	5.3	1097	7	US-11-056-355B-69789	Sequence 69790, A	223	71	5.1	531	6	US-10-449-902-31417	Sequence 31417, A
151	73.5	5.3	1128	7	US-11-056-355B-69788	Sequence 69789, A	224	71	5.1	569	7	US-11-056-355B-89699	Sequence 89699, A
152	73	5.2	203	7	US-11-056-355B-72695	Sequence 69788, A	225	71	5.1	569	7	US-11-056-355B-93455	Sequence 93455, A
153	73	5.2	332	6	US-10-953-349-22929	Sequence 72695, A	226	71	5.1	649	7	US-11-056-355B-90301	Sequence 90301, A
154	73	5.2	332	7	US-11-056-355B-54621	Sequence 54621, A	227	71	5.1	649	7	US-11-056-355B-94057	Sequence 94057, A
155	73	5.2	348	6	US-11-056-355B-54620	Sequence 54619, A	228	71	5.1	687	7	US-11-218-716-8	Sequence 8, Appli
156	73	5.2	348	7	US-11-056-355B-72694	Sequence 54620, A	229	71	5.1	692	7	US-11-056-355B-90300	Sequence 90300, A
157	73	5.2	353	7	US-11-056-355B-72694	Sequence 72694, A	230	71	5.1	692	7	US-11-056-355B-94056	Sequence 94056, A
158	73	5.2	355	6	US-10-953-349-22927	Sequence 22927, A	231	71	5.1	693	6	US-10-505-928-678	Sequence 678, App
159	73	5.2	355	7	US-11-056-355B-54619	Sequence 22927, A	232	71	5.1	693	7	US-11-218-716-2	Sequence 2, Appli
160	73	5.2	365	6	US-10-449-902-51917	Sequence 54619, A	233	71	5.1	693	7	US-11-218-716-4	Sequence 4, Appli
161	73	5.2	401	7	US-11-056-355B-72693	Sequence 51917, A	234	71	5.1	693	7	US-11-218-716-6	Sequence 6, Appli
162	73	5.2	458	7	US-11-217-529-3	Sequence 72693, A	235	71	5.1	733	7	US-11-056-355B-90299	Sequence 90299, A
163	73	5.2	458	7	US-11-056-355B-13955	Sequence 13955, A	236	71	5.1	733	7	US-11-056-355B-94055	Sequence 94055, A
164	73	5.2	458	7	US-11-056-355B-18291	Sequence 18291, A	237	71	5.1	819	6	US-10-449-902-46126	Sequence 46126, A
165	72.5	5.2	283	6	US-10-449-902-43863	Sequence 43863, A	238	71	5.1	819	6	US-10-449-902-46754	Sequence 46754, A
166	72.5	5.2	274	7	US-11-056-355B-52749	Sequence 52749, A	239	71	5.1	918	7	US-11-275-181-6	Sequence 6, Appli
167	72.5	5.2	290	7	US-11-056-355B-52748	Sequence 52748, A	240	70.5	5.1	286	7	US-11-056-355B-39702	Sequence 39702, A
168	72.5	5.2	316	7	US-11-056-355B-70765	Sequence 70765, A	241	70.5	5.1	286	7	US-11-330-403-7378	Sequence 7378, Ap
169	72.5	5.2	407	7	US-11-330-403-11369	Sequence 11369, A	242	70.5	5.1	287	6	US-10-953-349-9179	Sequence 9179, Ap
170	72.5	5.2	421	6	US-10-953-349-16497	Sequence 16497, A	243	70.5	5.1	287	6	US-10-953-349-9711	Sequence 9711, Ap
171	72.5	5.2	423	6	US-10-953-349-16496	Sequence 16496, A	244	70.5	5.1	287	6		

245	70.5	5.1	287	7	US-11-056-355B-29005	Sequence 29005, A	318	69.5	5.0	466	6	US-10-449-902-54312	Sequence 54312, A
246	70.5	5.1	287	7	US-11-056-355B-32595	Sequence 32595, A	319	69.5	5.0	472	7	US-11-275-264-2	Sequence 2, Appli
247	70.5	5.1	287	7	US-11-056-355B-41696	Sequence 41696, A	320	69.5	5.0	472	7	US-11-330-403-4886	Sequence 4886, Ap
248	70.5	5.1	287	7	US-11-056-355B-44798	Sequence 44798, A	321	69.5	5.0	472	7	US-11-330-403-15117	Sequence 15117, A
249	70.5	5.1	287	7	US-11-056-355B-84600	Sequence 84600, A	322	69.5	5.0	472	7	US-11-330-403-17706	Sequence 17706, A
250	70.5	5.1	287	7	US-11-056-355B-84604	Sequence 84604, A	323	69.5	5.0	492	7	US-11-330-403-4693	Sequence 4693, Ap
251	70.5	5.1	287	7	US-11-056-355B-98275	Sequence 98275, A	324	69.5	5.0	493	6	US-10-953-349-2205	Sequence 2205, Ap
252	70.5	5.1	287	7	US-11-056-355B-108389	Sequence 108389,	325	69.5	5.0	493	7	US-11-056-355B-40482	Sequence 40482, A
253	70.5	5.1	287	7	US-11-056-355B-109514	Sequence 109514,	326	69.5	5.0	493	7	US-11-056-355B-102249	Sequence 102249,
254	70.5	5.1	287	7	US-11-056-355B-119628	Sequence 119628,	327	69.5	5.0	493	7	US-11-056-355B-113488	Sequence 113488,
255	70.5	5.1	319	7	US-11-377-517-6	Sequence 6, Appli	328	69.5	5.0	507	7	US-11-330-403-9565	Sequence 9565, Ap
256	70.5	5.1	319	7	US-11-377-517-7	Sequence 7, Appli	329	69.5	5.0	515	7	US-11-330-403-533	Sequence 533, App
257	70.5	5.1	419	6	US-10-471-571A-4350	Sequence 4350, Ap	330	69.5	5.0	525	7	US-11-330-403-15816	Sequence 15816, A
258	70.5	5.1	454	7	US-11-056-355B-91799	Sequence 91799, A	331	69.5	5.0	617	7	US-11-056-355B-42359	Sequence 42359, A
259	70.5	5.1	454	7	US-11-056-355B-95555	Sequence 95555, A	332	69.5	5.0	619	7	US-11-056-355B-42358	Sequence 42358, A
260	70.5	5.1	515	7	US-11-056-355B-81260	Sequence 81260, A	333	69.5	5.0	630	7	US-11-056-355B-42357	Sequence 42357, A
261	70.5	5.1	520	7	US-11-174-307B-5508	Sequence 5508, Ap	334	69.5	5.0	781	7	US-11-330-403-2056	Sequence 2056, Ap
262	70.5	5.1	520	7	US-11-296-657-4	Sequence 4, Appli	335	69.5	5.0	794	7	US-11-330-403-11306	Sequence 11306, A
263	70.5	5.1	525	7	US-11-056-355B-81259	Sequence 81259, A	336	69	5.0	285	7	US-11-330-403-15938	Sequence 15938, A
264	70.5	5.1	533	7	US-11-056-355B-81258	Sequence 81258, A	337	69	5.0	321	7	US-11-332-138-2	Sequence 2, Appli
265	70.5	5.1	546	7	US-11-056-355B-77798	Sequence 77798, A	338	69	5.0	328	7	US-11-056-355B-52854	Sequence 52854, A
266	70.5	5.1	549	7	US-11-056-355B-87887	Sequence 87887, A	339	69	5.0	353	7	US-11-056-355B-77764	Sequence 77764, A
267	70.5	5.1	553	6	US-10-517-552-10	Sequence 10, Appl	340	69	5.0	353	7	US-11-056-355B-85908	Sequence 85908, A
268	70.5	5.1	564	7	US-11-056-355B-87886	Sequence 87886, A	341	69	5.0	366	6	US-10-961-569-2	Sequence 2, Appli
269	70.5	5.1	594	7	US-11-056-355B-87885	Sequence 87885, A	342	69	5.0	366	6	US-10-961-569-20	Sequence 20, Appl
270	70.5	5.1	619	7	US-11-312-958-46	Sequence 46, Appl	343	69	5.0	371	7	US-11-056-355B-77763	Sequence 77763, A
271	70.5	5.1	687	7	US-11-341-947-2	Sequence 2, Appli	344	69	5.0	371	7	US-11-056-355B-85907	Sequence 85907, A
272	70.5	5.1	687	7	US-11-218-716-10	Sequence 10, Appl	345	69	5.0	382	7	US-11-056-355B-90765	Sequence 90765, A
273	70.5	5.1	823	7	US-11-330-403-609	Sequence 609, App	346	69	5.0	382	7	US-11-056-355B-94521	Sequence 94521, A
274	70.5	5.1	850	7	US-11-056-355B-75830	Sequence 75830, A	347	69	5.0	389	7	US-11-056-355B-77762	Sequence 77762, A
275	70.5	5.1	861	7	US-11-056-355B-100179	Sequence 100179,	348	69	5.0	398	6	US-10-449-902-47833	Sequence 47833, A
276	70.5	5.1	861	7	US-11-056-355B-111418	Sequence 111418,	349	69	5.0	458	7	US-11-056-355B-85906	Sequence 85906, A
277	70.5	5.1	870	7	US-11-056-355B-75829	Sequence 75829, A	350	69	5.0	471	6	US-10-449-902-38797	Sequence 38797, A
278	70.5	5.1	881	7	US-11-056-355B-100178	Sequence 100178,	351	69	5.0	479	7	US-11-330-403-4766	Sequence 4766, Ap
279	70.5	5.1	881	7	US-11-056-355B-111417	Sequence 111417,	352	69	5.0	487	6	US-10-471-571A-3798	Sequence 3798, Ap
280	70.5	5.1	886	6	US-10-449-902-43638	Sequence 43638, A	353	69	5.0	492	6	US-10-511-937-2952	Sequence 2952, Ap
281	70.5	5.1	886	6	US-10-449-902-46619	Sequence 46619, A	354	69	5.0	502	6	US-10-545-334-4	Sequence 4, Appli
282	70.5	5.1	1058	7	US-11-056-355B-75828	Sequence 75828, A	355	69	5.0	502	6	US-10-545-334-6	Sequence 6, Appli
283	70.5	5.1	1069	7	US-11-056-355B-100177	Sequence 100177,	356	69	5.0	527	7	US-11-174-307B-3816	Sequence 3816, Ap
284	70.5	5.1	1069	7	US-11-056-355B-111416	Sequence 111416,	357	69	5.0	527	7	US-11-233-089-42	Sequence 42, Appl
285	70	5.0	173	6	US-10-953-349-11257	Sequence 11257, A	358	69	5.0	781	7	US-11-330-403-8852	Sequence 8852, Ap
286	70	5.0	173	7	US-11-056-355B-46645	Sequence 46645, A	359	69	5.0	1095	7	US-11-226-554-95	Sequence 95, Appl
287	70	5.0	177	6	US-10-953-349-11256	Sequence 11256, A	360	69	5.0	1095	7	US-11-226-554-96	Sequence 96, Appl
288	70	5.0	177	7	US-11-056-355B-46644	Sequence 46644, A	361	69	5.0	1095	7	US-11-248-718-95	Sequence 95, Appl
289	70	5.0	208	7	US-11-030-653-8	Sequence 8, Appli	362	69	5.0	1095	7	US-11-248-718-96	Sequence 96, Appl
290	70	5.0	218	7	US-11-056-355B-102310	Sequence 102310,	363	68.5	4.9	226	7	US-11-056-355B-39379	Sequence 39379, A
291	70	5.0	218	7	US-11-056-355B-113549	Sequence 113549,	364	68.5	4.9	252	7	US-11-056-355B-97611	Sequence 97611, A
292	70	5.0	262	6	US-10-449-902-31380	Sequence 31380, A	365	68.5	4.9	252	7	US-11-056-355B-108850	Sequence 108850,
293	70	5.0	262	6	US-10-449-902-51444	Sequence 51444, A	366	68.5	4.9	263	7	US-11-056-355B-39378	Sequence 39378, A
294	70	5.0	262	6	US-10-449-902-54914	Sequence 54914, A	367	68.5	4.9	329	7	US-11-056-355B-45626	Sequence 45626, A
295	70	5.0	288	7	US-11-330-403-8004	Sequence 8004, Ap	368	68.5	4.9	329	7	US-11-056-355B-50568	Sequence 50568, A
296	70	5.0	296	7	US-11-330-403-2246	Sequence 2246, Ap	369	68.5	4.9	343	7	US-11-056-355B-45625	Sequence 45625, A
297	70	5.0	364	6	US-10-953-349-16498	Sequence 16498, A	370	68.5	4.9	343	7	US-11-056-355B-50567	Sequence 50567, A
298	70	5.0	364	6	US-10-449-902-49967	Sequence 49967, A	371	68.5	4.9	385	7	US-11-056-355B-24553	Sequence 24553, A
299	70	5.0	512	7	US-11-330-403-12827	Sequence 12827, A	372	68.5	4.9	407	7	US-11-330-403-12810	Sequence 12810, A
300	70	5.0	518	7	US-11-330-403-8770	Sequence 8770, Ap	373	68.5	4.9	415	7	US-11-056-355B-78941	Sequence 78941, A
301	70	5.0	526	6	US-10-953-349-7169	Sequence 7169, Ap	374	68.5	4.9	431	7	US-11-330-403-1168	Sequence 1168, Ap
302	70	5.0	778	6	US-10-449-902-43100	Sequence 43100, A	375	68.5	4.9	435	6	US-10-953-349-7171	Sequence 7171, Ap
303	70	5.0	778	6	US-10-449-902-43438	Sequence 43438, A	376	68.5	4.9	436	6	US-10-953-349-7170	Sequence 7170, Ap
304	70	5.0	905	6	US-10-449-902-31457	Sequence 31457, A	377	68.5	4.9	448	7	US-11-056-355B-78940	Sequence 78940, A
305	69.5	5.0	202	6	US-10-953-349-2415	Sequence 2415, Ap	378	68.5	4.9	454	7	US-11-056-355B-78939	Sequence 78939, A
306	69.5	5.0	202	7	US-11-056-355B-27404	Sequence 27404, A	379	68.5	4.9	483	7	US-11-056-355B-100606	Sequence 100606,
307	69.5	5.0	202	7	US-11-056-355B-74656	Sequence 74656, A	380	68.5	4.9	483	7	US-11-056-355B-111845	Sequence 111845,
308	69.5	5.0	226	7	US-11-056-355B-101410	Sequence 101410,	381	68.5	4.9	502	7	US-11-056-355B-100605	Sequence 100605,
309	69.5	5.0	226	7	US-11-056-355B-112649	Sequence 112649,	382	68.5	4.9	502	7	US-11-056-355B-111844	Sequence 111844,
310	69.5	5.0	247	6	US-10-953-349-2414	Sequence 2414, Ap	383	68.5	4.9	509	7	US-11-056-355B-100604	Sequence 100604,
311	69.5	5.0	247	7	US-11-056-355B-27403	Sequence 27403, A	384	68.5	4.9	509	7	US-11-056-355B-111843	Sequence 111843,
312	69.5	5.0	247	7	US-11-056-355B-74655	Sequence 74655, A	385	68.5	4.9	518	6	US-10-449-902-31365	Sequence 31365, A
313	69.5	5.0	261	7	US-11-056-355B-101409	Sequence 101409,	386	68.5	4.9	592	6	US-10-449-902-38524	Sequence 38524, A
314	69.5	5.0	261	7	US-11-056-355B-112648	Sequence 112648,	387	68.5	4.9	867	7	US-11-056-355B-75940	Sequence 75940, A
315	69.5	5.0	263	7	US-11-056-355B-101408	Sequence 101408,	388	68.5	4.9	884	7	US-11-056-355B-91295	Sequence 91295, A
316	69.5	5.0	263	7	US-11-056-355B-112647	Sequence 112647,	389	68.5	4.9	884	7	US-11-056-355B-95051	Sequence 95051, A
317	69.5	5.0	287	7	US-11-330-403-6433	Sequence 6433, Ap	390	68.5	4.9	907	7	US-11-056-355B-75747	Sequence 75747, A



391	68.5	4.9	925	7	US-11-056-355B-100336	Sequence 100336,	464	67.5	4.8	1054	7	US-11-056-355B-47978	Sequence 47978, A
392	68.5	4.9	925	7	US-11-056-355B-111575	Sequence 111575,	465	67.5	4.8	1054	7	US-11-056-355B-48216	Sequence 48216, A
393	68.5	4.9	939	7	US-11-056-355B-75939	Sequence 75939, A	466	67.5	4.8	1065	7	US-11-056-355B-37224	Sequence 37224, A
394	68.5	4.9	949	7	US-11-056-355B-75746	Sequence 75746, A	467	67.5	4.8	1065	7	US-11-056-355B-47977	Sequence 47977, A
395	68.5	4.9	956	7	US-11-056-355B-91294	Sequence 91294, A	468	67.5	4.8	1065	7	US-11-056-355B-48215	Sequence 48215, A
396	68.5	4.9	956	7	US-11-056-355B-95050	Sequence 95050, A	469	67.5	4.8	1092	6	US-10-449-902-53776	Sequence 53776, A
397	68.5	4.9	967	7	US-11-056-355B-100335	Sequence 100335,	470	67.5	4.8	1201	7	US-11-273-537-31	Sequence 31, Appl
398	68.5	4.9	967	7	US-11-056-355B-111574	Sequence 111574,	471	67.5	4.8	1263	6	US-10-471-571A-5118	Sequence 5118, Ap
399	68.5	4.9	1066	7	US-11-056-355B-75745	Sequence 75745, A	472	67	4.8	250	6	US-10-449-902-40088	Sequence 40088, A
400	68.5	4.9	1067	7	US-11-056-355B-75938	Sequence 75938, A	473	67	4.8	258	7	US-11-056-355B-5154	Sequence 5154, Ap
401	68.5	4.9	1081	7	US-11-325-276-29	Sequence 29, Appl	474	67	4.8	258	7	US-11-056-355B-6210	Sequence 6210, Ap
402	68.5	4.9	1084	7	US-11-056-355B-91293	Sequence 91293, A	475	67	4.8	264	7	US-11-056-355B-5153	Sequence 5153, Ap
403	68.5	4.9	1084	7	US-11-056-355B-95049	Sequence 95049, A	476	67	4.8	264	7	US-11-056-355B-6209	Sequence 6209, Ap
404	68.5	4.9	1084	7	US-11-056-355B-100334	Sequence 100334,	477	67	4.8	265	7	US-11-056-355B-24744	Sequence 24744, A
405	68.5	4.9	1084	7	US-11-056-355B-111573	Sequence 111573,	478	67	4.8	290	6	US-10-471-571A-498	Sequence 498, App
406	68.5	4.9	1084	7	US-11-325-276-24	Sequence 24, Appl	479	67	4.8	292	7	US-11-056-355B-6208	Sequence 6208, Ap
407	68	4.9	217	7	US-11-056-355B-73050	Sequence 73050, A	480	67	4.8	293	7	US-11-330-403-1176	Sequence 1176, Ap
408	68	4.9	265	6	US-10-449-902-54848	Sequence 54848, A	481	67	4.8	293	7	US-11-330-403-1251	Sequence 1251, Ap
409	68	4.9	290	6	US-10-953-349-25004	Sequence 25004, A	482	67	4.8	293	7	US-11-330-403-5047	Sequence 5047, Ap
410	68	4.9	290	6	US-11-056-355B-55296	Sequence 55296, A	483	67	4.8	297	7	US-11-056-355B-5152	Sequence 5152, Ap
411	68	4.9	305	6	US-10-471-571A-2352	Sequence 2352, Ap	484	67	4.8	313	6	US-10-953-349-27376	Sequence 27376, A
412	68	4.9	355	7	US-11-404-939-475	Sequence 475, App	485	67	4.8	313	6	US-11-056-355B-63128	Sequence 63128, A
413	68	4.9	369	7	US-11-056-355B-78288	Sequence 78288, A	486	67	4.8	314	6	US-10-953-349-27375	Sequence 27375, A
414	68	4.9	372	6	US-10-953-349-25003	Sequence 25003, A	487	67	4.8	314	6	US-10-953-349-28001	Sequence 28001, A
415	68	4.9	372	7	US-11-056-355B-55295	Sequence 55295, A	488	67	4.8	314	6	US-11-056-355B-63127	Sequence 63127, A
416	68	4.9	443	7	US-11-056-355B-100239	Sequence 100239,	489	67	4.8	334	7	US-11-056-355B-89673	Sequence 89673, A
417	68	4.9	443	7	US-11-056-355B-111478	Sequence 111478,	490	67	4.8	334	7	US-11-056-355B-93429	Sequence 93429, A
418	68	4.9	457	7	US-11-330-403-927	Sequence 927, App	491	67	4.8	340	6	US-10-953-349-28000	Sequence 28000, A
419	68	4.9	458	6	US-10-449-902-51682	Sequence 51682, A	492	67	4.8	345	7	US-11-330-403-3922	Sequence 3922, Ap
420	68	4.9	458	6	US-10-449-902-54211	Sequence 54211, A	493	67	4.8	356	7	US-11-056-355B-89672	Sequence 89672, A
421	68	4.9	458	7	US-11-317-789A-438	Sequence 438, App	494	67	4.8	356	7	US-11-056-355B-93428	Sequence 93428, A
422	68	4.9	461	7	US-11-330-403-10235	Sequence 10235, A	495	67	4.8	357	6	US-10-953-349-27374	Sequence 27374, A
423	68	4.9	464	7	US-11-330-403-7208	Sequence 7208, Ap	496	67	4.8	357	7	US-11-056-355B-63126	Sequence 63126, A
424	68	4.9	486	6	US-10-449-902-50373	Sequence 50373, A	497	67	4.8	358	7	US-11-056-355B-89671	Sequence 89671, A
425	68	4.9	486	7	US-11-330-403-18338	Sequence 18338, A	498	67	4.8	358	7	US-11-056-355B-93427	Sequence 93427, A
426	68	4.9	493	7	US-11-330-403-7774	Sequence 7774, Ap	499	67	4.8	363	6	US-10-449-902-56364	Sequence 56364, A
427	68	4.9	506	7	US-11-056-355B-100238	Sequence 100238,	500	67	4.8	370	6	US-10-505-928-672	Sequence 672, App
428	68	4.9	506	7	US-11-056-355B-111477	Sequence 111477,	501	67	4.8	370	6	US-10-449-902-55544	Sequence 55544, A
429	68	4.9	510	6	US-10-449-902-46896	Sequence 46896, A	502	67	4.8	397	6	US-10-505-405-22	Sequence 22, Appl
430	68	4.9	532	7	US-11-330-403-1984	Sequence 1984, Ap	503	67	4.8	398	7	US-11-056-355B-2956	Sequence 2956, Ap
431	68	4.9	624	7	US-11-056-355B-100237	Sequence 100237,	504	67	4.8	398	7	US-11-317-789A-439	Sequence 439, App
432	68	4.9	624	7	US-11-056-355B-111476	Sequence 111476,	505	67	4.8	408	6	US-10-953-349-5885	Sequence 5885, Ap
433	68	4.9	722	7	US-11-330-403-8355	Sequence 8355, Ap	506	67	4.8	408	7	US-11-056-355B-34976	Sequence 34976, A
434	68	4.9	905	6	US-10-449-902-42984	Sequence 42984, A	507	67	4.8	408	7	US-11-056-355B-99387	Sequence 99387, A
435	67.5	4.8	171	7	US-11-056-355B-5480	Sequence 5480, Ap	508	67	4.8	408	7	US-11-056-355B-110626	Sequence 110626,
436	67.5	4.8	293	7	US-11-330-403-15524	Sequence 15524, A	509	67	4.8	408	7	US-11-330-403-334	Sequence 334, App
437	67.5	4.8	304	6	US-10-471-571A-4038	Sequence 4038, Ap	510	67	4.8	413	6	US-10-953-349-24222	Sequence 24222, A
438	67.5	4.8	336	7	US-11-178-538-4	Sequence 4, Appl	511	67	4.8	413	7	US-10-953-349-25275	Sequence 25275, A
439	67.5	4.8	365	6	US-10-953-349-28815	Sequence 28815, A	512	67	4.8	414	7	US-11-056-355B-25274	Sequence 25274, A
440	67.5	4.8	365	7	US-11-056-355B-68532	Sequence 68532, A	513	67	4.8	429	6	US-10-953-349-24221	Sequence 24221, A
441	67.5	4.8	389	6	US-10-953-349-28814	Sequence 28814, A	514	67	4.8	431	6	US-10-953-349-24220	Sequence 24220, A
442	67.5	4.8	389	7	US-11-056-355B-68531	Sequence 68531, A	515	67	4.8	459	7	US-11-056-355B-2955	Sequence 2955, Ap
443	67.5	4.8	443	7	US-11-056-355B-37552	Sequence 37552, A	516	67	4.8	459	7	US-11-317-789A-437	Sequence 437, App
444	67.5	4.8	443	7	US-11-330-403-16503	Sequence 16503, A	517	67	4.8	462	7	US-11-056-355B-25273	Sequence 25273, A
445	67.5	4.8	457	7	US-11-056-355B-41660	Sequence 41660, A	518	67	4.8	473	6	US-10-953-349-11576	Sequence 11576, A
446	67.5	4.8	458	7	US-11-056-355B-41659	Sequence 41659, A	519	67	4.8	473	7	US-11-056-355B-48903	Sequence 48903, A
447	67.5	4.8	463	7	US-11-330-403-19149	Sequence 19149, A	520	67	4.8	474	7	US-11-056-355B-78061	Sequence 78061, A
448	67.5	4.8	473	6	US-10-449-902-47556	Sequence 47556, A	521	67	4.8	474	7	US-11-056-355B-85172	Sequence 85172, A
449	67.5	4.8	479	7	US-11-056-355B-83856	Sequence 83856, A	522	67	4.8	491	6	US-10-449-902-44498	Sequence 44498, A
450	67.5	4.8	490	6	US-10-449-902-45547	Sequence 45547, A	523	67	4.8	491	7	US-11-056-355B-84959	Sequence 84959, A
451	67.5	4.8	501	7	US-11-056-355B-41658	Sequence 41658, A	524	67	4.8	507	6	US-10-953-349-25186	Sequence 25186, A
452	67.5	4.8	511	7	US-11-056-355B-83855	Sequence 83855, A	525	67	4.8	508	6	US-10-953-349-25185	Sequence 25185, A
453	67.5	4.8	514	7	US-11-056-355B-37551	Sequence 37551, A	526	67	4.8	520	7	US-11-056-355B-2954	Sequence 2954, Ap
454	67.5	4.8	515	7	US-11-056-355B-83854	Sequence 83854, A	527	67	4.8	521	7	US-11-056-355B-84958	Sequence 84958, A
455	67.5	4.8	532	7	US-11-056-355B-37550	Sequence 37550, A	528	67	4.8	524	6	US-10-953-349-11575	Sequence 11575, A
456	67.5	4.8	578	6	US-10-471-571A-2774	Sequence 2774, Ap	529	67	4.8	524	7	US-11-056-355B-48902	Sequence 48902, A
457	67.5	4.8	717	7	US-11-293-697-3828	Sequence 3828, Ap	530	67	4.8	524	7	US-11-056-355B-78060	Sequence 78060, A
458	67.5	4.8	754	6	US-10-518-941-28	Sequence 28, Appl	531	67	4.8	527	7	US-11-056-355B-84957	Sequence 84957, A
459	67.5	4.8	801	6	US-10-471-571A-258	Sequence 258, App	532	67	4.8	552	6	US-10-953-349-25184	Sequence 25184, A
460	67.5	4.8	959	7	US-11-056-355B-37226	Sequence 37226, A	533	67	4.8	555	7	US-11-056-355B-78306	Sequence 78306, A
461	67.5	4.8	959	7	US-11-056-355B-47979	Sequence 47979, A	534	67	4.8	559	6	US-10-953-349-11574	Sequence 11574, A
462	67.5	4.8	959	7	US-11-056-355B-48217	Sequence 48217, A	535	67	4.8	559	7	US-11-056-355B-48901	Sequence 48901, A
463	67.5	4.8	1054	7	US-11-056-355B-37225	Sequence 37225, A	536	67	4.8	567	7	US-11-056-355B-78305	Sequence 78305, A

537	67	4.8	602	7	US-11-056-355B-78059	Sequence 78059, A	610	66	4.7	320	7	US-11-226-554-139	Sequence 139, App
538	67	4.8	626	7	US-11-056-355B-38198	Sequence 38198, A	611	66	4.7	320	7	US-11-248-718-139	Sequence 139, App
539	67	4.8	626	7	US-11-056-355B-77180	Sequence 77180, A	612	66	4.7	350	6	US-10-449-902-53738	Sequence 53738, A
540	67	4.8	626	7	US-11-056-355B-104394	Sequence 104394, A	613	66	4.7	360	6	US-10-449-902-53506	Sequence 53506, A
541	67	4.8	626	7	US-11-056-355B-115633	Sequence 115633, A	614	66	4.7	368	6	US-10-449-902-47641	Sequence 47641, A
542	67	4.8	644	7	US-11-056-355B-38197	Sequence 38197, A	615	66	4.7	390	6	US-10-471-571A-2582	Sequence 2582, Ap
543	67	4.8	644	7	US-11-056-355B-77179	Sequence 77179, A	616	66	4.7	402	7	US-11-330-403-860	Sequence 860, App
544	67	4.8	644	7	US-11-056-355B-104393	Sequence 104393, A	617	66	4.7	432	6	US-10-471-571A-822	Sequence 822, App
545	67	4.8	644	7	US-11-056-355B-115632	Sequence 115632, A	618	66	4.7	440	6	US-10-449-902-31378	Sequence 31378, A
546	67	4.8	657	6	US-10-449-902-44861	Sequence 44861, A	619	66	4.7	459	7	US-11-330-403-15410	Sequence 15410, A
547	67	4.8	674	7	US-11-330-403-12193	Sequence 12193, A	620	66	4.7	460	6	US-10-953-349-5285	Sequence 5285, Ap
548	67	4.8	695	7	US-11-056-355B-38196	Sequence 38196, A	621	66	4.7	460	7	US-11-330-403-10226	Sequence 10226, A
549	67	4.8	695	7	US-11-056-355B-77178	Sequence 77178, A	622	66	4.7	462	6	US-10-953-349-5284	Sequence 5284, Ap
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551	67	4.8	695	7	US-11-056-355B-115631	Sequence 115631, A	624	66	4.7	513	6	US-10-953-349-5283	Sequence 5283, Ap
552	67	4.8	742	7	US-11-056-355B-78304	Sequence 78304, A	625	66	4.7	624	6	US-10-449-902-40952	Sequence 40952, A
553	67	4.8	967	6	US-10-505-405-2	Sequence 2, Appli	626	66	4.7	646	7	US-11-021-837-58	Sequence 58, Appli
554	67	4.8	967	6	US-10-505-405-6	Sequence 6, Appli	627	66	4.7	666	7	US-11-056-355B-72327	Sequence 72327, A
555	67	4.8	1332	7	US-11-301-094-6	Sequence 6, Appli	628	66	4.7	694	7	US-11-056-355B-71616	Sequence 71616, A
556	67	4.8	1359	7	US-11-270-796-22	Sequence 22, Appl	629	66	4.7	695	7	US-11-330-403-13159	Sequence 13159, A
557	66.5	4.8	241	7	US-11-347-766-18	Sequence 18, Appl	630	66	4.7	741	7	US-11-056-355B-72326	Sequence 72326, A
558	66.5	4.8	242	7	US-11-056-355B-1540	Sequence 1540, Ap	631	66	4.7	769	7	US-11-056-355B-71615	Sequence 71615, A
559	66.5	4.8	263	6	US-10-449-902-39161	Sequence 39161, A	632	66	4.7	790	6	US-10-449-902-52717	Sequence 52717, A
560	66.5	4.8	270	6	US-10-449-902-34690	Sequence 34690, A	633	66	4.7	853	7	US-11-056-355B-72325	Sequence 72325, A
561	66.5	4.8	287	6	US-10-471-571A-4460	Sequence 4460, Ap	634	66	4.7	881	7	US-11-056-355B-71614	Sequence 71614, A
562	66.5	4.8	297	7	US-11-330-403-6313	Sequence 6313, Ap	635	66	4.7	1333	7	US-11-270-796-3	Sequence 3, Appli
563	66.5	4.8	302	7	US-11-056-355B-1539	Sequence 1539, Ap	636	65.5	4.7	137	6	US-10-449-902-52012	Sequence 52012, A
564	66.5	4.8	310	7	US-11-056-355B-1538	Sequence 1538, Ap	637	65.5	4.7	186	6	US-10-449-902-31572	Sequence 31572, A
565	66.5	4.8	370	6	US-10-449-902-56226	Sequence 56226, A	638	65.5	4.7	194	6	US-10-449-902-43714	Sequence 43714, A
566	66.5	4.8	378	7	US-11-056-355B-3915	Sequence 3915, Ap	639	65.5	4.7	237	7	US-11-105-233-65	Sequence 65, Appl
567	66.5	4.8	391	6	US-10-953-349-21132	Sequence 21132, A	640	65.5	4.7	242	6	US-10-449-902-44536	Sequence 44536, A
568	66.5	4.8	396	7	US-11-056-355B-3914	Sequence 3914, Ap	641	65.5	4.7	286	7	US-11-056-355B-28777	Sequence 28777, A
569	66.5	4.8	403	6	US-10-953-349-21131	Sequence 21131, A	642	65.5	4.7	286	7	US-11-056-355B-32367	Sequence 32367, A
570	66.5	4.8	428	6	US-10-953-349-21130	Sequence 21130, A	643	65.5	4.7	300	6	US-10-449-902-40217	Sequence 40217, A
571	66.5	4.8	499	6	US-10-471-571A-3194	Sequence 3194, Ap	644	65.5	4.7	307	7	US-11-056-355B-70623	Sequence 70623, A
572	66.5	4.8	512	7	US-11-330-403-5812	Sequence 5812, Ap	645	65.5	4.7	311	7	US-11-056-355B-70622	Sequence 70622, A
573	66.5	4.8	513	7	US-11-330-403-8839	Sequence 8839, Ap	646	65.5	4.7	329	7	US-11-056-355B-70621	Sequence 70621, A
574	66.5	4.8	520	6	US-10-471-571A-5356	Sequence 5356, Ap	647	65.5	4.7	344	7	US-11-056-355B-69786	Sequence 69786, A
575	66.5	4.8	546	6	US-10-449-902-49911	Sequence 49911, A	648	65.5	4.7	352	6	US-10-449-902-35485	Sequence 35485, A
576	66.5	4.8	553	6	US-10-517-552-1	Sequence 1, Appli	649	65.5	4.7	355	6	US-10-516-032-8	Sequence 8, Appli
577	66.5	4.8	599	7	US-11-293-697-3454	Sequence 3454, Ap	650	65.5	4.7	360	6	US-10-449-902-36130	Sequence 36130, A
578	66.5	4.8	616	7	US-11-056-355B-100223	Sequence 100223, A	651	65.5	4.7	360	6	US-10-449-902-47417	Sequence 47417, A
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580	66.5	4.8	661	6	US-10-449-902-33093	Sequence 33093, A	653	65.5	4.7	381	7	US-11-056-355B-19589	Sequence 19589, A
581	66.5	4.8	661	6	US-10-449-902-51012	Sequence 51012, A	654	65.5	4.7	383	7	US-11-056-355B-3277	Sequence 3277, Ap
582	66.5	4.8	685	7	US-11-056-355B-100222	Sequence 100222, A	655	65.5	4.7	390	7	US-11-056-355B-97731	Sequence 97731, A
583	66.5	4.8	685	7	US-11-056-355B-111461	Sequence 111461, A	656	65.5	4.7	390	7	US-11-056-355B-108970	Sequence 108970, A
584	66.5	4.8	696	6	US-10-539-228-574	Sequence 574, App	657	65.5	4.7	396	7	US-11-330-403-11889	Sequence 11889, A
585	66.5	4.8	717	7	US-11-056-355B-100221	Sequence 100221, A	658	65.5	4.7	397	7	US-11-330-403-4722	Sequence 4722, Ap
586	66.5	4.8	717	7	US-11-056-355B-111460	Sequence 111460, A	659	65.5	4.7	398	7	US-11-197-712-288	Sequence 288, App
587	66.5	4.8	837	6	US-10-449-902-45332	Sequence 45332, A	660	65.5	4.7	401	6	US-10-953-349-31569	Sequence 31569, A
588	66.5	4.8	899	7	US-11-377-884-48	Sequence 4419, A	661	65.5	4.7	401	6	US-10-515-283A-5	Sequence 5, Appli
589	66.5	4.8	941	6	US-10-449-902-44419	Sequence 79003, A	662	65.5	4.7	401	7	US-11-264-737-54	Sequence 54, Appl
590	66.5	4.8	957	7	US-11-056-355B-79003	Sequence 79003, A	663	65.5	4.7	401	7	US-11-265-761-42	Sequence 42, Appl
591	66.5	4.8	960	7	US-11-256-173-15	Sequence 15, Appl	664	65.5	4.7	401	7	US-11-056-355B-66509	Sequence 66509, A
592	66.5	4.8	960	7	US-11-056-355B-70322	Sequence 70322, A	665	65.5	4.7	404	7	US-11-056-355B-19588	Sequence 19588, A
593	66.5	4.8	970	7	US-11-056-355B-79002	Sequence 79002, A	666	65.5	4.7	428	7	US-11-033-553-3	Sequence 3, Appli
594	66.5	4.8	973	7	US-11-056-355B-70321	Sequence 70321, A	667	65.5	4.7	431	7	US-11-330-403-12302	Sequence 12302, A
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597	66.5	4.8	1148	7	US-11-325-276-4	Sequence 4, Appli	670	65.5	4.7	464	7	US-11-330-403-3415	Sequence 3415, Ap
598	66.5	4.8	1704	7	US-11-289-102-341	Sequence 341, App	671	65.5	4.7	464	7	US-11-330-403-7852	Sequence 7852, Ap
599	66	4.7	285	7	US-11-056-355B-28819	Sequence 28819, A	672	65.5	4.7	464	7	US-11-330-403-10134	Sequence 10134, A
600	66	4.7	285	7	US-11-056-355B-32409	Sequence 32409, A	673	65.5	4.7	483	7	US-11-251-208-459	Sequence 459, App
601	66	4.7	285	7	US-11-056-355B-35822	Sequence 35822, A	674	65.5	4.7	494	7	US-11-330-403-18433	Sequence 18433, A
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603	66	4.7	285	7	US-11-056-355B-102377	Sequence 102377, A	676	65.5	4.7	517	6	US-10-471-571A-3562	Sequence 3562, Ap
604	66	4.7	285	7	US-11-056-355B-113616	Sequence 113616, A	677	65.5	4.7	654	6	US-10-471-571A-1262	Sequence 1262, Ap
605	66	4.7	290	7	US-11-330-403-15987	Sequence 15987, A	678	65.5	4.7	792	7	US-11-330-403-9551	Sequence 9551, Ap
606	66	4.7	306	7	US-11-056-355B-52855	Sequence 52855, A	679	65.5	4.7	989	6	US-10-449-902-53376	Sequence 53376, A
607	66	4.7	306	7	US-11-056-355B-35821	Sequence 35821, A	680	65.5	4.7	994	6	US-10-449-902-43721	Sequence 43721, A
608	66	4.7	306	7	US-11-056-355B-102376	Sequence 102376, A	681	65.5	4.7	1073	6	US-10-449-902-47216	Sequence 47216, A
609	66	4.7	306	7	US-11-056-355B-113615	Sequence 113615, A	682	65	4.7	206	6	US-10-953-349-3843	Sequence 3843, Ap

683	65	4.7	206	7	US-11-056-355B-59163	Sequence 59163, A	756	64.5	4.6	343	6	US-10-540-898-807	Sequence 807, App
684	65	4.7	229	7	US-11-056-355B-22221	Sequence 22221, A	757	64.5	4.6	353	7	US-11-251-208-81	Sequence 81, Appl
685	65	4.7	248	7	US-11-330-403-2930	Sequence 2930, Ap	758	64.5	4.6	355	7	US-11-056-355B-24739	Sequence 24739, A
686	65	4.7	251	6	US-10-953-349-3842	Sequence 3842, Ap	759	64.5	4.6	355	7	US-11-056-355B-106000	Sequence 106000,
687	65	4.7	254	6	US-10-953-349-3841	Sequence 3841, Ap	760	64.5	4.6	355	7	US-11-056-355B-117239	Sequence 117239,
688	65	4.7	263	7	US-11-056-355B-59162	Sequence 59162, A	761	64.5	4.6	361	7	US-11-056-355B-24738	Sequence 24738, A
689	65	4.7	265	7	US-11-330-403-16166	Sequence 16166, A	762	64.5	4.6	361	7	US-11-056-355B-105999	Sequence 105999,
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691	65	4.7	276	7	US-11-330-403-12903	Sequence 12903, A	764	64.5	4.6	366	6	US-10-953-349-38438	Sequence 38438, A
692	65	4.7	282	7	US-11-056-355B-8878	Sequence 8878, Ap	765	64.5	4.6	370	7	US-11-056-355B-24554	Sequence 24554, A
693	65	4.7	285	6	US-10-953-349-28002	Sequence 28002, A	766	64.5	4.6	386	6	US-10-953-349-4908	Sequence 4908, Ap
694	65	4.7	290	7	US-11-056-355B-83235	Sequence 83235, A	767	64.5	4.6	394	7	US-11-330-403-6926	Sequence 6926, Ap
695	65	4.7	291	7	US-11-056-355B-105425	Sequence 105425,	768	64.5	4.6	395	6	US-10-953-349-38437	Sequence 38437, A
696	65	4.7	291	7	US-11-056-355B-116664	Sequence 116664,	769	64.5	4.6	401	7	US-11-330-403-19198	Sequence 19198, A
697	65	4.7	298	7	US-11-293-697-3724	Sequence 3724, Ap	770	64.5	4.6	421	7	US-11-330-403-1202	Sequence 1202, Ap
698	65	4.7	302	7	US-11-056-355B-59161	Sequence 59161, A	771	64.5	4.6	426	7	US-11-199-489A-8	Sequence 8, Appl1
699	65	4.7	319	7	US-11-056-355B-105424	Sequence 105424,	772	64.5	4.6	429	7	US-11-330-403-3369	Sequence 3369, Ap
700	65	4.7	319	7	US-11-056-355B-116663	Sequence 116663,	773	64.5	4.6	438	6	US-10-449-902-53385	Sequence 53385, A
701	65	4.7	330	7	US-11-056-355B-83234	Sequence 83234, A	774	64.5	4.6	469	6	US-10-953-349-4907	Sequence 4907, Ap
702	65	4.7	332	6	US-10-471-571A-3224	Sequence 3224, Ap	775	64.5	4.6	472	7	US-11-330-403-13903	Sequence 13903, A
703	65	4.7	354	6	US-10-953-349-3453	Sequence 3453, Ap	776	64.5	4.6	484	6	US-10-953-349-4906	Sequence 4906, Ap
704	65	4.7	354	7	US-11-056-355B-35815	Sequence 35815, A	777	64.5	4.6	501	7	US-11-056-355B-56971	Sequence 56971, A
705	65	4.7	363	7	US-11-056-355B-11036	Sequence 11036, A	778	64.5	4.6	509	7	US-11-330-403-11453	Sequence 11453, A
706	65	4.7	372	6	US-10-953-349-3452	Sequence 3452, Ap	779	64.5	4.6	513	6	US-10-471-571A-1992	Sequence 1992, Ap
707	65	4.7	372	7	US-11-056-355B-35814	Sequence 35814, A	780	64.5	4.6	548	6	US-10-471-571A-4310	Sequence 4310, Ap
708	65	4.7	400	6	US-10-953-349-10675	Sequence 10675, A	781	64.5	4.6	604	7	US-11-330-403-10471	Sequence 10471, A
709	65	4.7	400	7	US-11-056-355B-37669	Sequence 37669, A	782	64.5	4.6	805	6	US-10-449-902-47265	Sequence 47265, A
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711	65	4.7	409	7	US-11-174-307B-4288	Sequence 4288, Ap	784	64.5	4.6	823	7	US-11-330-403-2570	Sequence 2570, Ap
712	65	4.7	418	6	US-10-953-349-10674	Sequence 10674, A	785	64.5	4.6	823	7	US-11-330-403-5019	Sequence 5019, Ap
713	65	4.7	418	7	US-11-056-355B-37668	Sequence 37668, A	786	64.5	4.6	823	7	US-11-330-403-5025	Sequence 5025, Ap
714	65	4.7	418	7	US-11-056-355B-49562	Sequence 49562, A	787	64.5	4.6	823	7	US-11-330-403-18196	Sequence 18196, A
715	65	4.7	418	7	US-11-056-355B-76798	Sequence 76798, A	788	64.5	4.6	2292	7	US-11-335-891-25	Sequence 25, Appl
716	65	4.7	432	6	US-10-953-349-10673	Sequence 10673, A	789	64	4.6	196	6	US-10-449-902-31753	Sequence 31753, A
717	65	4.7	432	7	US-11-056-355B-37667	Sequence 37667, A	790	64	4.6	247	6	US-10-953-349-24149	Sequence 24149, A
718	65	4.7	432	7	US-11-056-355B-49561	Sequence 49561, A	791	64	4.6	250	6	US-10-449-902-28625	Sequence 28625, A
719	65	4.7	432	7	US-11-056-355B-76797	Sequence 76797, A	792	64	4.6	250	6	US-10-449-902-30233	Sequence 30233, A
720	65	4.7	449	7	US-11-330-403-679	Sequence 679, App	793	64	4.6	250	6	US-10-449-902-47000	Sequence 47000, A
721	65	4.7	451	7	US-11-056-355B-76796	Sequence 76796, A	794	64	4.6	268	7	US-11-056-355B-91496	Sequence 91496, A
722	65	4.7	458	7	US-11-226-908-8	Sequence 8, Appl	795	64	4.6	268	7	US-11-056-355B-95252	Sequence 95252, A
723	65	4.7	459	6	US-10-953-349-3451	Sequence 3451, Ap	796	64	4.6	271	6	US-10-953-349-24148	Sequence 24148, A
724	65	4.7	459	7	US-11-056-355B-35813	Sequence 35813, A	797	64	4.6	278	6	US-10-953-349-27783	Sequence 27783, A
725	65	4.7	459	7	US-11-330-403-15584	Sequence 15584, A	798	64	4.6	278	7	US-11-056-355B-64684	Sequence 64684, A
726	65	4.7	462	7	US-11-226-908-6	Sequence 6, Appl	799	64	4.6	279	7	US-11-056-355B-91495	Sequence 91495, A
727	65	4.7	470	7	US-11-056-355B-70546	Sequence 70546, A	800	64	4.6	279	7	US-11-056-355B-95251	Sequence 95251, A
728	65	4.7	482	7	US-11-056-355B-70545	Sequence 70545, A	801	64	4.6	280	7	US-11-056-355B-86637	Sequence 86637, A
729	65	4.7	500	7	US-11-056-355B-97327	Sequence 97327, A	802	64	4.6	281	7	US-11-056-355B-86636	Sequence 86636, A
730	65	4.7	518	6	US-10-196-749-72	Sequence 72, Appl	803	64	4.6	282	7	US-11-056-355B-86635	Sequence 86635, A
731	65	4.7	518	7	US-11-056-355B-97326	Sequence 97326, A	804	64	4.6	292	7	US-11-330-403-1541	Sequence 1541, Ap
732	65	4.7	540	7	US-11-330-403-711	Sequence 711, App	805	64	4.6	296	7	US-11-249-111-103	Sequence 103, App
733	65	4.7	555	7	US-11-330-403-6828	Sequence 6828, Ap	806	64	4.6	296	7	US-11-056-355B-82159	Sequence 82159, A
734	65	4.7	581	7	US-11-251-465-18	Sequence 18, Appl	807	64	4.6	297	7	US-11-056-355B-82158	Sequence 82158, A
735	65	4.7	614	7	US-11-330-403-8768	Sequence 8768, Ap	808	64	4.6	298	7	US-11-056-355B-82157	Sequence 82157, A
736	65	4.7	662	6	US-10-471-571A-5102	Sequence 5102, Ap	809	64	4.6	330	7	US-11-056-355B-13532	Sequence 13532, A
737	65	4.7	866	6	US-10-449-902-52724	Sequence 52724, A	810	64	4.6	334	6	US-10-953-349-27782	Sequence 27782, A
738	64.5	4.6	195	6	US-10-953-349-37920	Sequence 37920, A	811	64	4.6	334	7	US-11-056-355B-64683	Sequence 64683, A
739	64.5	4.6	211	6	US-10-953-349-37919	Sequence 37919, A	812	64	4.6	339	6	US-10-449-902-30871	Sequence 30871, A
740	64.5	4.6	233	6	US-10-449-902-35792	Sequence 35792, A	813	64	4.6	351	6	US-10-449-902-55826	Sequence 55826, A
741	64.5	4.6	286	7	US-11-056-355B-97694	Sequence 97694, A	814	64	4.6	357	6	US-10-471-571A-5444	Sequence 5444, Ap
742	64.5	4.6	286	7	US-11-056-355B-108933	Sequence 108933,	815	64	4.6	364	7	US-11-056-355B-13531	Sequence 13531, A
743	64.5	4.6	287	6	US-10-953-349-2977	Sequence 2977, Ap	816	64	4.6	366	6	US-10-953-349-17831	Sequence 17831, A
744	64.5	4.6	287	7	US-11-056-355B-26812	Sequence 26812, A	817	64	4.6	366	6	US-10-449-902-47698	Sequence 47698, A
745	64.5	4.6	287	7	US-11-056-355B-87735	Sequence 87735, A	818	64	4.6	366	6	US-10-449-902-47755	Sequence 47755, A
746	64.5	4.6	291	7	US-11-330-403-5805	Sequence 5805, Ap	819	64	4.6	367	6	US-10-953-349-27781	Sequence 27781, A
747	64.5	4.6	305	6	US-10-953-349-38439	Sequence 38439, A	820	64	4.6	367	7	US-11-056-355B-64682	Sequence 64682, A
748	64.5	4.6	323	7	US-11-330-403-3732	Sequence 3732, Ap	821	64	4.6	376	7	US-11-056-355B-13530	Sequence 13530, A
749	64.5	4.6	327	7	US-11-330-403-18251	Sequence 18251, A	822	64	4.6	394	6	US-10-535-928A-41	Sequence 41, Appl
750	64.5	4.6	328	6	US-10-527-788-69	Sequence 69, Appl	823	64	4.6	403	7	US-11-197-712-249	Sequence 249, App
751	64.5	4.6	335	7	US-11-056-355B-24740	Sequence 24740, A	824	64	4.6	409	7	US-11-330-403-11557	Sequence 11557, A
752	64.5	4.6	335	7	US-11-056-355B-106001	Sequence 106001,	825	64	4.6	424	7	US-11-056-355B-57320	Sequence 57320, A
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754	64.5	4.6	343	6	US-10-540-898-803	Sequence 803, App	827	64	4.6	439	7	US-11-056-355B-57319	Sequence 57319, A
755	64.5	4.6	343	6	US-10-540-898-805	Sequence 805, App	828	64	4.6	460	7	US-11-330-403-12867	Sequence 12867, A

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832	64	4.6	490	7	US-11-330-403-1544	Sequence 1544, Ap	905	63.5	4.6	426	7	US-11-056-355B-27623	Sequence 27623, A
833	64	4.6	493	6	US-10-953-349-10425	Sequence 10425, A	906	63.5	4.6	426	7	US-11-056-355B-31213	Sequence 31213, A
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835	64	4.6	493	7	US-11-056-355B-85104	Sequence 85104, A	908	63.5	4.6	435	7	US-11-296-657-72	Sequence 72, Appl
836	64	4.6	509	6	US-10-953-349-10424	Sequence 10424, A	909	63.5	4.6	435	7	US-11-056-355B-52482	Sequence 52482, A
837	64	4.6	509	7	US-11-056-355B-49279	Sequence 49279, A	910	63.5	4.6	441	6	US-10-449-902-40892	Sequence 40892, A
838	64	4.6	509	7	US-11-056-355B-85103	Sequence 85103, A	911	63.5	4.6	448	6	US-10-449-902-44009	Sequence 44009, A
839	64	4.6	509	7	US-11-330-403-18529	Sequence 18529, A	912	63.5	4.6	448	6	US-10-449-902-52836	Sequence 52836, A
840	64	4.6	520	7	US-11-330-403-9849	Sequence 9849, Ap	913	63.5	4.6	448	7	US-11-317-789A-435	Sequence 435, App
841	64	4.6	548	7	US-11-056-355B-57318	Sequence 57318, A	914	63.5	4.6	449	7	US-11-056-355B-70725	Sequence 70725, A
842	64	4.6	553	7	US-11-330-403-1906	Sequence 1906, Ap	915	63.5	4.6	449	7	US-11-056-355B-74956	Sequence 74956, A
843	64	4.6	578	7	US-11-330-403-15368	Sequence 15368, A	916	63.5	4.6	451	7	US-11-330-403-4120	Sequence 4120, Ap
844	64	4.6	586	6	US-10-449-902-39151	Sequence 39151, A	917	63.5	4.6	460	7	US-11-056-355B-40263	Sequence 40263, A
845	64	4.6	588	7	US-11-330-403-14209	Sequence 14209, A	918	63.5	4.6	460	7	US-11-056-355B-70724	Sequence 70724, A
846	64	4.6	618	7	US-11-330-403-7153	Sequence 7153, Ap	919	63.5	4.6	460	7	US-11-056-355B-74955	Sequence 74955, A
847	64	4.6	658	7	US-11-174-307B-3680	Sequence 3680, Ap	920	63.5	4.6	488	7	US-11-242-505A-30	Sequence 30, Appl
848	64	4.6	664	7	US-11-056-355B-46978	Sequence 46978, A	921	63.5	4.6	488	7	US-11-404-939-561	Sequence 561, App
849	64	4.6	666	6	US-10-953-349-3549	Sequence 3549, Ap	922	63.5	4.6	510	7	US-11-330-403-15785	Sequence 15785, A
850	64	4.6	673	7	US-11-056-355B-46977	Sequence 46977, A	923	63.5	4.6	605	7	US-11-330-403-4015	Sequence 4015, Ap
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852	64	4.6	682	6	US-10-449-902-56273	Sequence 56273, A	925	63.5	4.6	2292	7	US-11-335-891-26	Sequence 26, Appl
853	64	4.6	690	6	US-10-953-349-3548	Sequence 3548, Ap	926	63.5	4.6	2292	7	US-11-335-891-28	Sequence 28, Appl
854	64	4.6	808	6	US-10-449-902-44460	Sequence 44460, A	927	63	4.5	185	6	US-10-953-349-15254	Sequence 15254, A
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858	64	4.6	902	6	US-10-953-349-3547	Sequence 3547, Ap	931	63	4.5	238	6	US-10-449-902-48149	Sequence 48149, A
859	64	4.6	919	7	US-11-056-355B-75346	Sequence 75346, A	932	63	4.5	247	6	US-10-953-349-15253	Sequence 15253, A
860	64	4.6	926	7	US-11-056-355B-73565	Sequence 73565, A	933	63	4.5	247	6	US-10-953-349-37011	Sequence 37011, A
861	64	4.6	954	7	US-11-056-355B-75345	Sequence 75345, A	934	63	4.5	247	7	US-11-056-355B-55918	Sequence 55918, A
862	64	4.6	1488	7	US-11-330-403-15631	Sequence 15631, A	935	63	4.5	259	6	US-10-522-356-22	Sequence 22, Appl
863	64	4.6	1551	7	US-11-377-884-46	Sequence 46, Appl	936	63	4.5	271	6	US-10-953-349-23075	Sequence 23075, A
864	64	4.6	2301	7	US-11-335-891-30	Sequence 30, Appl	937	63	4.5	287	6	US-10-953-349-23074	Sequence 23074, A
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866	63.5	4.6	218	6	US-10-504-973-24	Sequence 24, Appl	939	63	4.5	290	7	US-11-340-429-4	Sequence 4, Appli
867	63.5	4.6	269	6	US-10-471-571A-4828	Sequence 4828, Ap	940	63	4.5	290	7	US-11-378-707-14	Sequence 14, Appl
868	63.5	4.6	269	6	US-10-449-902-48668	Sequence 48668, A	941	63	4.5	290	7	US-11-346-468-2	Sequence 2, Appli
869	63.5	4.6	273	7	US-11-056-355B-45627	Sequence 45627, A	942	63	4.5	293	7	US-11-330-403-7498	Sequence 7498, Ap
870	63.5	4.6	273	7	US-11-056-355B-50569	Sequence 50569, A	943	63	4.5	299	6	US-10-953-349-15252	Sequence 15252, A
871	63.5	4.6	273	7	US-11-056-355B-27087	Sequence 27087, A	944	63	4.5	299	7	US-11-056-355B-55917	Sequence 55917, A
872	63.5	4.6	280	6	US-11-056-355B-62842	Sequence 62842, A	945	63	4.5	311	6	US-10-471-571A-3480	Sequence 3480, Ap
873	63.5	4.6	284	6	US-10-953-349-27086	Sequence 27086, A	946	63	4.5	333	7	US-11-056-355B-84881	Sequence 84881, A
874	63.5	4.6	284	7	US-11-056-355B-62841	Sequence 62841, A	947	63	4.5	350	7	US-11-056-355B-84880	Sequence 84880, A
875	63.5	4.6	286	6	US-10-953-349-9374	Sequence 9374, Ap	948	63	4.5	358	7	US-11-056-355B-84879	Sequence 84879, A
876	63.5	4.6	286	7	US-11-056-355B-25360	Sequence 25360, A	949	63	4.5	364	7	US-11-293-697-4612	Sequence 4612, Ap
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878	63.5	4.6	289	7	US-11-056-355B-2594	Sequence 2594, Ap	951	63	4.5	410	7	US-11-174-307B-3942	Sequence 3942, Ap
879	63.5	4.6	295	6	US-10-953-349-23478	Sequence 23478, A	952	63	4.5	413	6	US-10-953-349-38771	Sequence 38771, A
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881	63.5	4.6	315	7	US-11-056-355B-27625	Sequence 27625, A	954	63	4.5	416	6	US-10-449-902-47396	Sequence 47396, A
882	63.5	4.6	315	7	US-11-056-355B-31215	Sequence 31215, A	955	63	4.5	418	6	US-10-953-349-23073	Sequence 23073, A
883	63.5	4.6	318	6	US-10-471-571A-3052	Sequence 3052, Ap	956	63	4.5	436	7	US-11-330-403-10416	Sequence 10416, A
884	63.5	4.6	348	6	US-10-953-349-23477	Sequence 23477, A	957	63	4.5	462	6	US-10-953-349-38769	Sequence 38769, A
885	63.5	4.6	353	7	US-11-264-784-63	Sequence 63, Appl	958	63	4.5	463	6	US-10-449-902-53826	Sequence 53826, A
886	63.5	4.6	353	7	US-11-265-761-76	Sequence 96, Appl	959	63	4.5	486	6	US-10-449-902-43179	Sequence 43179, A
887	63.5	4.6	353	7	US-11-265-761-76	Sequence 76, Appl	960	63	4.5	486	7	US-11-330-403-6277	Sequence 6277, Ap
888	63.5	4.6	354	6	US-10-953-349-23476	Sequence 23476, A	961	63	4.5	498	7	US-11-330-403-2313	Sequence 2313, Ap
889	63.5	4.6	356	7	US-11-384-847-7	Sequence 7, Appli	962	63	4.5	512	6	US-10-471-571A-2270	Sequence 2270, Ap
890	63.5	4.6	357	6	US-10-953-349-23681	Sequence 23681, A	963	63	4.5	527	6	US-10-539-228-787	Sequence 787, App
891	63.5	4.6	358	7	US-11-330-403-10791	Sequence 10791, A	964	63	4.5	530	7	US-11-296-657-10	Sequence 10, Appl
892	63.5	4.6	374	6	US-10-953-349-23680	Sequence 23680, A	965	63	4.5	539	7	US-11-330-403-12434	Sequence 12434, A
893	63.5	4.6	374	7	US-11-330-403-10027	Sequence 10027, A	966	63	4.5	576	6	US-10-449-902-52631	Sequence 52631, A
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895	63.5	4.6	394	7	US-11-330-403-2843	Sequence 2843, Ap	968	63	4.5	590	6	US-10-449-902-49011	Sequence 49011, A
896	63.5	4.6	402	6	US-10-449-902-47229	Sequence 47229, A	969	63	4.5	610	7	US-11-330-403-16759	Sequence 16759, A
897	63.5	4.6	402	6	US-10-449-902-55879	Sequence 55879, A	970	63	4.5	658	6	US-10-953-349-4215	Sequence 4215, Ap
898	63.5	4.6	403	6	US-10-471-571A-2620	Sequence 2620, Ap	971	63	4.5	660	6	US-10-953-349-4214	Sequence 4214, Ap
899	63.5	4.6	411	7	US-11-056-355B-40265	Sequence 40265, A	972	63	4.5	661	6	US-10-953-349-4213	Sequence 4213, Ap
900	63.5	4.6	412	7	US-11-056-355B-40264	Sequence 40264, A	973	63	4.5	691	7	US-11-056-355B-44819	Sequence 44819, A
901	63.5	4.6	412	7	US-11-056-355B-70726	Sequence 70726, A	974	63	4.5	691	7	US-11-056-355B-48027	Sequence 48027, A



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976	63	4.5	697	7	US-11-056-355B-44818	Sequence 44818, A	1049	62.5	4.5	579	6	US-10-449-902-56026	Sequence 56026, A
977	63	4.5	697	7	US-11-056-355B-48026	Sequence 48026, A	1050	62.5	4.5	583	7	US-11-330-403-18668	Sequence 18668, A
978	63	4.5	735	7	US-11-293-697-4426	Sequence 4426, Ap	1051	62.5	4.5	587	7	US-11-292-951-4	Sequence 4, Appli
979	63	4.5	772	7	US-11-056-355B-44817	Sequence 44817, A	1052	62.5	4.5	595	6	US-10-517-552-9	Sequence 9, Appli
980	63	4.5	772	7	US-11-056-355B-48025	Sequence 48025, A	1053	62.5	4.5	595	6	US-10-517-420-35	Sequence 35, Appl
981	63	4.5	777	7	US-11-330-403-10510	Sequence 10510, A	1054	62.5	4.5	597	7	US-11-330-403-15178	Sequence 15178, A
982	63	4.5	822	7	US-11-330-403-7212	Sequence 7212, Ap	1055	62.5	4.5	616	7	US-11-056-355B-86327	Sequence 86327, A
983	63	4.5	822	7	US-11-330-403-17883	Sequence 17883, A	1056	62.5	4.5	632	7	US-11-056-355B-72810	Sequence 72810, A
984	63	4.5	828	7	US-11-330-403-12723	Sequence 12723, A	1057	62.5	4.5	640	6	US-10-953-349-24506	Sequence 24506, A
985	63	4.5	1016	6	US-10-449-902-43193	Sequence 43193, A	1058	62.5	4.5	644	6	US-10-517-420-44	Sequence 44, Appl
986	63	4.5	1016	6	US-10-449-902-45738	Sequence 45738, A	1059	62.5	4.5	644	6	US-10-517-420-45	Sequence 45, Appl
987	63	4.5	1215	6	US-10-953-349-8001	Sequence 8001, Ap	1060	62.5	4.5	652	6	US-10-517-420-27	Sequence 27, Appl
988	63	4.5	1215	7	US-11-056-355B-39533	Sequence 39533, A	1061	62.5	4.5	652	6	US-10-517-420-41	Sequence 41, Appl
989	63	4.5	1215	7	US-11-056-355B-106299	Sequence 106299,	1062	62.5	4.5	659	7	US-11-056-355B-81954	Sequence 81954, A
990	63	4.5	1215	7	US-11-056-355B-117538	Sequence 117538,	1063	62.5	4.5	671	6	US-10-517-420-33	Sequence 33, Appl
991	63	4.5	1355	6	US-10-953-349-8000	Sequence 8000, Ap	1064	62.5	4.5	685	6	US-10-517-420-31	Sequence 31, Appl
992	63	4.5	1355	7	US-11-056-355B-39532	Sequence 39532, A	1065	62.5	4.5	694	6	US-10-517-420-46	Sequence 46, Appl
993	63	4.5	1355	7	US-11-056-355B-106298	Sequence 106298,	1066	62.5	4.5	694	6	US-10-517-420-47	Sequence 47, Appl
994	63	4.5	1355	7	US-11-056-355B-117537	Sequence 117537,	1067	62.5	4.5	694	6	US-10-517-420-48	Sequence 48, Appl
995	63	4.5	1514	6	US-10-953-349-7999	Sequence 7999, Ap	1068	62.5	4.5	698	6	US-10-953-349-4543	Sequence 4543, Ap
996	63	4.5	1514	7	US-11-133-075-9	Sequence 9, Appli	1069	62.5	4.5	709	6	US-10-953-349-4542	Sequence 4542, Ap
997	63	4.5	1514	7	US-11-056-355B-39531	Sequence 39531, A	1070	62.5	4.5	725	6	US-10-953-349-4541	Sequence 4541, Ap
998	63	4.5	1514	7	US-11-056-355B-106297	Sequence 106297,	1071	62.5	4.5	725	7	US-11-056-355B-81953	Sequence 81953, A
999	63	4.5	1514	7	US-11-056-355B-117536	Sequence 117536,	1072	62.5	4.5	755	7	US-11-056-355B-43896	Sequence 43896, A
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1001	62.5	4.5	239	7	US-11-115-024-2	Sequence 2, Appli	1074	62.5	4.5	919	7	US-11-302-678-62	Sequence 62, Appl
1002	62.5	4.5	255	7	US-11-319-952-75	Sequence 75, Appl	1075	62.5	4.5	995	6	US-10-471-571A-3910	Sequence 3910, Ap
1003	62.5	4.5	260	7	US-11-330-403-14497	Sequence 14497, A	1076	62.5	4.5	1092	6	US-10-449-902-53812	Sequence 53812, A
1004	62.5	4.5	261	7	US-11-319-952-79	Sequence 79, Appl	1077	62.5	4.5	1094	7	US-11-174-307B-298	Sequence 298, App
1005	62.5	4.5	286	6	US-10-449-902-50826	Sequence 50826, A	1078	62.5	4.5	1165	7	US-11-325-276-8	Sequence 8, Appli
1006	62.5	4.5	289	6	US-10-449-902-32900	Sequence 32900, A	1079	62.5	4.5	2516	7	US-11-070-573-25	Sequence 25, Appl
1007	62.5	4.5	295	7	US-11-330-403-17934	Sequence 17934, A	1080	62.5	4.5	2671	6	US-10-505-928-784	Sequence 784, App
1008	62.5	4.5	306	7	US-11-174-307B-2978	Sequence 2978, Ap	1081	62	4.5	189	7	US-11-056-355B-95803	Sequence 95803, A
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1010	62.5	4.5	323	6	US-10-449-902-49373	Sequence 49373, A	1083	62	4.5	202	7	US-11-056-355B-95802	Sequence 95802, A
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1012	62.5	4.5	332	7	US-11-297-134-48	Sequence 48, Appl	1085	62	4.5	203	7	US-11-056-355B-9906	Sequence 9906, Ap
1013	62.5	4.5	335	7	US-11-303-558-12	Sequence 12, Appl	1086	62	4.5	211	6	US-10-471-571A-808	Sequence 808, App
1014	62.5	4.5	336	7	US-11-174-307B-4360	Sequence 4360, Ap	1087	62	4.5	279	7	US-11-056-355B-87147	Sequence 87147, A
1015	62.5	4.5	337	7	US-11-174-307B-5142	Sequence 5142, Ap	1088	62	4.5	279	7	US-11-330-403-5575	Sequence 5575, Ap
1016	62.5	4.5	373	7	US-11-330-403-10060	Sequence 10060, A	1089	62	4.5	282	7	US-11-330-403-12702	Sequence 12702, A
1017	62.5	4.5	382	7	US-11-056-355B-71017	Sequence 71017, A	1090	62	4.5	285	7	US-11-330-403-18570	Sequence 18570, A
1018	62.5	4.5	401	7	US-11-056-355B-71016	Sequence 71016, A	1091	62	4.5	292	7	US-11-330-403-14906	Sequence 14906, A
1019	62.5	4.5	417	7	US-11-056-355B-86329	Sequence 86329, A	1092	62	4.5	296	7	US-11-330-403-12766	Sequence 12766, A
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1021	62.5	4.5	451	6	US-10-471-571A-1946	Sequence 1946, Ap	1094	62	4.5	298	7	US-11-056-355B-84523	Sequence 84523, A
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1024	62.5	4.5	494	7	US-11-056-355B-71015	Sequence 71015, A	1097	62	4.5	328	6	US-10-527-788-53	Sequence 53, Appl
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1026	62.5	4.5	504	6	US-10-539-228-334	Sequence 334, App	1099	62	4.5	331	7	US-11-056-355B-64841	Sequence 64841, A
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1029	62.5	4.5	507	7	US-11-179-064B-22	Sequence 22, Appl	1102	62	4.5	350	6	US-10-449-902-33198	Sequence 33198, A
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1032	62.5	4.5	514	7	US-11-056-355B-72811	Sequence 72811, A	1105	62	4.5	357	7	US-11-056-355B-40834	Sequence 40834, A
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1034	62.5	4.5	523	7	US-11-056-355B-40912	Sequence 40912, A	1107	62	4.5	357	7	US-11-056-355B-111707	Sequence 111707,
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1128	62	4.5	400	7	US-11-056-355B-87146	Sequence 87146, A	1201	62	4.5	2227	7	US-11-409-670-12	Sequence 12, Appl
1129	62	4.5	402	7	US-11-330-403-7592	Sequence 7592, Ap	1202	62	4.5	2227	7	US-11-411-493-12	Sequence 12, Appl
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1131	62	4.5	410	7	US-11-293-697-3074	Sequence 3074, Ap	1204	61.5	4.4	140	7	US-11-056-355B-11087	Sequence 11087, A
1132	62	4.5	412	7	US-11-330-403-3157	Sequence 3157, Ap	1205	61.5	4.4	167	7	US-11-056-355B-75507	Sequence 75507, A
1133	62	4.5	415	7	US-11-056-355B-64839	Sequence 64839, A	1206	61.5	4.4	168	7	US-11-122-986-176	Sequence 176, App
1134	62	4.5	427	7	US-11-056-355B-87145	Sequence 87145, A	1207	61.5	4.4	168	7	US-11-122-986-178	Sequence 178, App
1135	62	4.5	432	7	US-11-056-355B-102003	Sequence 102003, A	1208	61.5	4.4	190	6	US-10-953-349-34819	Sequence 34819, A
1136	62	4.5	432	7	US-11-056-355B-113242	Sequence 113242, A	1209	61.5	4.4	190	7	US-11-056-355B-8413	Sequence 8413, Ap
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1138	62	4.5	436	7	US-11-056-355B-67493	Sequence 67493, A	1211	61.5	4.4	226	7	US-11-056-355B-68803	Sequence 68803, A
1139	62	4.5	440	7	US-11-056-355B-80868	Sequence 80868, A	1212	61.5	4.4	231	6	US-10-953-349-34818	Sequence 34818, A
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1142	62	4.5	443	7	US-11-056-355B-104208	Sequence 104208, A	1215	61.5	4.4	266	6	US-10-449-902-32147	Sequence 32147, A
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1166	62	4.5	518	7	US-11-330-403-3072	Sequence 3072, Ap	1239	61.5	4.4	322	7	US-11-056-355B-68801	Sequence 68801, A
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1171	62	4.5	557	7	US-11-330-403-2683	Sequence 2683, Ap	1244	61.5	4.4	358	7	US-11-024-545-54	Sequence 54, Appl
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1173	62	4.5	570	7	US-11-056-355B-70107	Sequence 70107, A	1246	61.5	4.4	358	7	US-11-251-466-28	Sequence 28, Appl
1174	62	4.5	572	7	US-11-330-403-2118	Sequence 2118, Ap	1247	61.5	4.4	358	7	US-11-254-173-44	Sequence 44, Appl
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1176	62	4.5	585	6	US-10-449-902-55150	Sequence 55150, A	1249	61.5	4.4	358	7	US-11-264-737-20	Sequence 20, Appl
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1193	62	4.5	884	6	US-10-449-902-41313	Sequence 41313, A	1266	61.5	4.4	449	6	US-10-449-902-53110	Sequence 53110, A

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1268	61.5	4.4	465	6	US-10-449-902-52165	Sequence 52165, A	1341	61	4.4	344	7	US-11-056-355B-8179	Sequence 8179, Ap
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1271	61.5	4.4	490	7	US-11-330-403-8766	Sequence 8766, Ap	1344	61	4.4	357	6	US-10-449-902-29928	Sequence 29928, A
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1274	61.5	4.4	498	7	US-11-330-403-12592	Sequence 12592, A	1347	61	4.4	360	7	US-11-056-355B-64645	Sequence 64645, A
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1276	61.5	4.4	512	7	US-11-056-355B-106720	Sequence 106720,	1349	61	4.4	367	6	US-10-471-571A-3160	Sequence 3160, Ap
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ALIGNMENTS

RESULT 1  
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; Sequence 10, Application US/10196749  
; Publication No. US20060094864A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
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; APPLICANT: Wood, William I.  
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
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; CURRENT APPLICATION NUMBER: US/10/196,749  
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Best Local Similarity 100.0%; Pred. No. 4.9e-117;  
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## RESULT 2

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; Sequence 2, Application US/11101316
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; GENERAL INFORMATION:
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYP
; TITLE OF INVENTION: UNDEREXPRESSED IN ME
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 2
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-2

```

```
Query Match      100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. NO. 4.9e-117;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	MW	FQ	Q	G	L	S	F	L	P	S	A	L	V	I	W	T	S	A	F	I	F	S	Y	T	A	V	T	L	H	H	I	D	P	A	L	P	Y	I	S	D	T	G	T	V	A	P	E	K	C	L	F	G	A	M	L	60			
Db	1	MW	FQ	Q	G	L	S	F	L	P	S	A	L	V	I	W	T	S	A	F	I	F	S	Y	T	A	V	T	L	H	H	I	D	P	A	L	P	Y	I	S	D	T	G	T	V	A	P	E	K	C	L	F	G	A	M	L	60			
QY	61	NIA	A	V	L	C	I	A	T	I	Y	V	R	Y	K	Q	V	H	A	L	S	P	E	E	N	V	I	K	N	K	A	G	L	V	L	G	I	L	S	C	L	G	I	S	I	V	A	N	F	Q	K	T	T	L	F	A	120			
Db	61	NIA	A	V	L	C	I	A	T	I	Y	V	R	Y	K	Q	V	H	A	L	S	P	E	E	N	V	I	K	N	K	A	G	L	V	L	G	I	L	S	C	L	G	I	S	I	V	A	N	F	Q	K	T	T	L	F	A	120			
QY	121	HV	S	G	A	V	L	T	F	G	M	S	L	Y	M	F	V	Q	T	I	L	S	Y	Q	M	P	K	I	H	G	K	Q	V	F	W	I	R	L	L	V	I	W	C	G	S	A	L	S	M	L	T	C	S	S	V	L	180			
Db	121	HV	S	G	A	V	L	T	F	G	M	S	L	Y	M	F	V	Q	T	I	L	S	Y	Q	M	P	K	I	H	G	K	Q	V	F	W	I	R	L	L	V	I	W	C	G	S	A	L	S	M	L	T	C	S	S	V	L	180			
QY	181	H	S	G	N	F	G	T	D	L	E	Q	K	L	H	N	P	E	D	K	G	Y	V	L	H	M	I	T	T	A	E	W	S	M	S	F	S	F	F	G	F	F	L	T	Y	I	R	D	F	Q	K	I	S	L	R	V	E	A	N	240

```

Db      181 HSGNFCTDLEQKLHWNPEDKGYVLHMTTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240
Qy      241 LHGLTLYDTAPCPINNERTRLLSRDI 266
        |||||
Db      241 LHGLTLYDTAPCPINNERTRLLSRDI 266

RESULT 3
US-11-376-673-2
; Sequence 2, Application US/11376673
; Publication No. US20060160186A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPRESSED IN STOMACH TUMOR AND
; TITLE OF INVENTION: LUNG TUMOR
; FILE REFERENCE: P3230R1C165C
; CURRENT APPLICATION NUMBER: US/11/376,673
; CURRENT FILING DATE: 2006-03-14
; PRIOR APPLICATION NUMBER: 10/063742
; PRIOR FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 2
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-376-673-2

```

```
Query Match          100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.9e-117;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	MW	FQ	Q	L	S	F	L	S	A	L	V	I	W	T	S	A	A	F	I	S	Y	I	T	A	V	T	L	H	I	D	P	A	L	P	Y	I	S	D	T	G	T	V	A	P	E	K	L	F	G	A	M	L	60					
Db	1	MW	FQ	Q	L	S	F	L	S	A	L	V	I	W	T	S	A	A	F	I	S	Y	I	T	A	V	T	L	H	I	D	P	A	L	P	Y	I	S	D	T	G	T	V	A	P	E	K	L	F	G	A	M	L	60					
QY	61	NIA	A	V	L	C	I	A	T	I	Y	V	R	Y	K	Q	V	H	A	L	S	P	E	E	N	V	I	I	K	N	K	A	G	L	V	L	G	I	L	S	C	L	G	L	S	I	V	A	N	F	O	K	T	T	L	F	A	120	
Db	61	NIA	A	V	L	C	I	A	T	I	Y	V	R	Y	K	Q	V	H	A	L	S	P	E	E	N	V	I	I	K	N	K	A	G	L	V	L	G	I	L	S	C	L	G	L	S	I	V	A	N	F	O	K	T	T	L	F	A	120	
QY	121	HV	S	G	A	V	L	T	F	G	M	S	L	Y	M	F	V	Q	T	I	S	Y	Q	M	P	K	I	H	G	K	Q	V	F	W	I	R	L	L	V	I	W	C	G	V	S	A	L	S	M	L	T	C	S	S	V	L	180		
Db	121	HV	S	G	A	V	L	T	F	G	M	S	L	Y	M	F	V	Q	T	I	S	Y	Q	M	P	K	I	H	G	K	Q	V	F	W	I	R	L	L	V	I	W	C	G	V	S	A	L	S	M	L	T	C	S	S	V	L	180		
QY	181	H	S	G	N	F	G	T	D	L	E	Q	K	L	H	N	P	E	D	K	G	Y	V	L	H	M	I	T	T	A	E	W	S	M	S	F	S	F	F	G	F	L	T	Y	I	R	D	F	O	K	I	S	L	R	V	E	A	N	240
Db	181	H	S	G	N	F	G	T	D	L	E	Q	K	L	H	N	P	E	D	K	G	Y	V	L	H	M	I	T	T	A	E	W	S	M	S	F	S	F	F	G	F	L	T	Y	I	R	D	F	O	K	I	S	L	R	V	E	A	N	240
QY	241	L	H	G	L	T	L	Y	D	T	A	P	C	P	I	N	N	E	R	T	R	L	L	S	R	D	I	266																															
Db	241	L	H	G	L	T	L	Y	D	T	A	P	C	P	I	N	N	E	R	T	R	L	L	S	R	D	I	266																															

## RESULT 4

```

US-11-293-697-2867
; Sequence 2867, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260

```



; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2867
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2867

Query Match 34.9%; Score 486.5; DB 7; Length 238;
Best Local Similarity 38.6%; Pred. No. 3.8e-36;
Matches 96; Conservative 53; Mismatches 79; Indels 21; Gaps 3;

Qy 1 MWWFOQLSFLPSALVIWTSAAFIPIYSITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLCFLRGMAFVPFLLVTWSSAAFIISYVAVLSGHVNPFLPYISDTGTTPESGIFGFI 60

Qy 61 NIAAVLCIATIIYRYKQV-----HALSPEENVIIKLNKAGLVGLGILSCLGLSIVANFQ 113
Db 61 NFSAPLGAATMYTRYKIVQKQNTCYFSTPVENLV-----SLVLGLVGCFGMGIVANFQ 114

Qy 114 KTTLFAAHVSGAVLTFGMGSLYMFVQTLISYQMOPKHGQVFWIRLLLVWCGVSALS 173
Db 115 ELAVPVHDGALLAFVCGVVYTLQSIISYKSCPDWNSLSTCHIRMVISAVSAAVIPM 174

Qy 174 LTCSSVLHSGNFGTDLQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKI 233
Db 175 IVCASLISI-----TKLEWNPREDYVYHVVSACEWTVAFGFIFPLTFIQDFQSV 226

Qy 234 SLRVEANLH 242
Db 227 TLRISTEIN 235

RESULT 5
US-11-395-249-66
; Sequence 66, Application US/11395249
; Publication No. US20060177904A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fectel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000103.6
; CURRENT APPLICATION NUMBER: US/11/395,249
; CURRENT FILING DATE: 2006-04-03
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-395-249-66

Query Match 10.9%; Score 151.5; DB 7; Length 437;
Best Local Similarity 26.8%; Pred. No. 6.7e-06;
Matches 57; Conservative 28; Mismatches 79; Indels 49; Gaps 8;

Qy 10 FLPSALVIW-----TSAAFIFS-----YITAVTLHHI-----DPA----- 39
Db 46 WLPSLMTAWILLPVLSLAFSITGIWTVYAMAVNMHHVCPVENWSYNESCFFDPAEQGGPK 105
Qy 40 -----LPYISDTGTVAPEKCLFGAMLNIAAVLCIATIIYRYKQVHALSPEENVIIKLN 92

Db 106 TCCTLDDVPLISKGSYPPESCFLSLIGNMGAFMVALICLLRYGQLLEQSRHSWV-----N 161
Qy 93 KAGLVGLSCLGLSIVANFQKTTTLFAAHVSGAVLTFGMGSLYMFVQTLISYQMOPKHG 152
Db 162 TTALITGCTNAAGLLVVGNFQVDHARSLHYVGAGVAFPAGLLFVCLHCLSPTKGPPRWT 221
Qy 153 -----KQVFWIRLLLVWCGV-SALSM--LTCS 177
Db 222 WLWPICEVCWLSSPLSPWSSVESLSMRVLSN 254

RESULT 6
US-11-293-697-4787
; Sequence 4787, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4787
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4787

Query Match 7.1%; Score 99; DB 7; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.13;
Matches 40; Conservative 26; Mismatches 77; Indels 28; Gaps 4;

Qy 64 AVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLGILSCLGLSIVANFQKTTLFAAHVS 123
Db 7 ALICL----LRYGQLLEQSRHSWV----NTTALITGCTNAAGLLVVGNFQVDHARSLHYV 58

Qy 124 GAVLTFGMGSLYMFVQTLISYQMOPKHGQVFWIRLLLVWCGVSALSMLTCSSVLHSG 183
Db 59 GAGVAFPAGLLFVCLHCLSYQGATAPLDLAVAYLR-----SVLAVIAFITLVLSG 109

Qy 184 NFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKIS 234
Db 110 VFFVHRESSQLQHG-----AALCEWVCVIDILIFYGTFSYBFGAVS 149

RESULT 7
US-11-056-355B-83608
; Sequence 83608, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 83608
; LENGTH: 303
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(303)
; OTHER INFORMATION: Ceres Seq. ID no. 12670984
US-11-056-355B-83608





QY	4	FOQGLSFPSALVWTSAAFI	FSYITAVTLHHIDPALP	--YISDTGTVAPEKCLF	GAML-	60
		:::	:::	:::	:::	
Db	44	FPSAVTYL--ALIPGR	TIPFAWNLITA--GYVEQ	TIPGMVWSIIGLL----	LFGKLE	93
QY	61	-----NIAAVLC-----	IATYVRYKQVHALSPEENV	IILNKA	GLVLGI	100
		::	::	:::	::	
Db	94	PLWGSBELSKFIFIVNL	STSACVFMTAIVLYYITQ	EIYLYTPFSGFY-----	GVLSGL	147
QY	101	LSCLGLSIVANFQKTTL	FAAHV-----SGAVLTF	FGMSLYMFVQILSYQM	QPKHGKQ	154
		:::	:::	:::	:::	
Db	148	L--VGIKQLLPDQELN	FLVKIKAKWIPSLVALIS	ILGSI--FIYDFMSY-LP	VLLFGMY	202
QY	155	VFWIRLLLVICGVSALS	MLTCCSVLHSGNFGTDL	EOKLHNPNEDKG	YVLHMITTAAEWS	214
		::	::	::	::	
Db	203	MSWIYLR-----	-----FOKRLETSLK	GDPSSE-----	-----	226
QY	215	MSFSFFGEFLTYYRDF	QKISLRV-----EANLH	GLTLYDTAPCP-----	INNERTR	260
		::	::	::	::	
Db	227	--FSFSFFPEFVRPFL	DPDIASVFHRLLCGRSD	ARGETL--DTSPLPGS	DSFEANRRR	282

## RESULT 11

US-10-449-902-35289  
; Sequence 35289, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

```

; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269

```

Query Match	6.3%	Score 88;	DB 6;	Length 932;
Best Local Similarity	25.2%	Pred. NO. 7.5;		
Matches 34;	Conservative 23;	Mismatches 38;	Indels 40;	Gaps 7;

Qy	90	KLKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFMGSGSLYMFVQOTILSYQMOPK	149
Db	500	KINASGQT---ARLGFNTIAT-----SATHYNG-ILEYNAHSLYGFSQAIATHQALQG	548
Qy	150	IHGKQVFWIRLLLVWCGVSALSMLTCSVLSHSGNFGTDLQKLAHWNPEDKG---YVLHM	206
Db	549	LQKRPF-----ILTRSTFVGSGAYAA-----HWTGDNKGITWENLRYS	586
Qy	207	ITTAAEWSMSFSFFG	221
Db	587	IST-----MLNFGIFG	597

## RESULT 12

US-10-449-902-55200  
; Sequence 55200, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.

```
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-11-178-538-37

Query Match      6.1%; Score 85.5; DB 7; Length 481;
Best Local Similarity 20.2%; Pred. No. 5.9;
Matches 60; Conservative 47; Mismatches 99; Indels 91; Gaps 16;

QY 18 WT-SAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIA-AVLCI----- 68
    ||| ||| : : : : : ||| : : : : : ||| : : : : :
Db 90 WTFYHAFFFAFTVCSTVG-----GNISP-TTFAGRMIMIAYSVIGIPVNGILF 137
    ||| ||| : : : : : ||| : : : : : ||| : : : : :
QY 69 -----ATIVVRYKQ-----VHALSPE-----ENVIIKLNKAGLVGLSCLGILS 107
    ||| ||| : : : : : ||| : : : : : ||| : : : : :
Db 138 AGLGEYFGRTEAIYRRYKKYKMSDTHYVPPQLGLITTVVIALIPGIALFLVLPVGVH 197
    ||| ||| : : : : : ||| : : : : : ||| : : : : :
QY 108 IV--ANFQKTTLFAAHVSGAVLTFGMSLYMFVQITLSYQMPKIHGKQVFWIRLLLVIV 165
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 LLRELGLSSISLYSYVT--ITTIGFGD---YVPTFGA--NQPKEFGGWFVYQIFVIVW 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 166 ----CGVSALSMLTCCSSVLHSGNFGTDLQKLLHN-----PEDKGYVLHMITT 209
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 FIFSLGYLVMIIMTFITRGLQSKLAY-LEQQLSSNLKATQNRIWSGVTKDVGYLRRMLNE 309
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 210 AAEWSMSFSFFGFELTYIRDFOKISLRVEA-----NLHGLTLYDTAPCPINNER 258
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 310 -----LYILKVKPVYTDVDIAYTLPRSNSCPDLSMYRVEPAPIPSRK 351
    : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: August 28, 2006, 17:41:52
Job time : 44 secs
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RESULT 14
US-10-471-571A-4918
; Sequence 4918, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4918
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(372)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-4918

Query Match      6.2%; Score 86; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 4;
Matches 47; Conservative 55; Mismatches 107; Indels 50; Gaps 8;

QY 1 MWWFQQLSFLPSALVI--WTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGA 58
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 IYFLIQGYSIIQLEILMASYGIAAFLS-----LYKEKCFKIC 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 MLNIAAVLCIATIVVRYKQVHALSPEENVIIKLNKAGLVGLSCLGILSIVANFQKTLF 118
    | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 NLKDSNKLAVVSEIFKIIIGLLLLYQNQYLIL-----VVAQILLGLSYSMMAGVD-TAII 116
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 AAHVSGAVLTFGMGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVWCGVSALSMLTCS 178
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 KRNIITNEKYVQNKSNSYMFSLLSIIIGSYLYGINIKWPIIMTGIF-SILTIIRCTL 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 VLHSGNFGTDLQKLLHNPEDKGYVLHMITTAAEWSMSFSF-----FGFELTYIRDFOKI 233
    | : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 VEN-----RELNLIGETKGIKKFKLPEEKFWILHVSFLRALILGFFIGFI----PI 222
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 SLRVEANLHGLTLYDTAPC 252
    : : : : : |
Db 223 NIYNDLKLNNLQFISVLT 241
    : : : : : |
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```
RESULT 15
US-11-178-538-37
; Sequence 37, Application US/11178538
; Publication No. US20060110792A1
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; TITLE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/11/178,538
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: .PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 481
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Title: US-10-006-867-2  
Perfect score: 1392  
Sequence: 1 MWFFQQLSFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Database : Published Applications\_AA\_Main:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
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2	1392	100.0	266 3 US-09-989-723-23 Sequence 23, Appl
3	1392	100.0	266 3 US-09-989-279-23 Sequence 23, Appl
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ALIGNMENTS

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; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC63  
; CURRENT APPLICATION NUMBER: US/09/989,722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;  
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RESULT 3

US-09-989-279-23

; Sequence 23, Application Us/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250



; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;  
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Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Pan, James  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C65  
; CURRENT APPLICATION NUMBER: US/09/989,727  
; CURRENT FILING DATE: 2001-11-19  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;  
Best Local Similarity 100.0%; Pred. No. 5.1e-127;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWWFQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

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Db 61 NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

Qy 121 HVSGAVLTFCGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSVL 180  
Db 121 HVSGAVLTFCGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSVL 180

Qy 181 HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKISLRVEAN 240  
Db 181 HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKISLRVEAN 240

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RESULT 5  
US-09-989-731-23  
; Sequence 23, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.



APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C70  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: US/09/989,731  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066770  
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PRIOR APPLICATION NUMBER: 60/075945  
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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Desnovers, Luc  
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; APPLICANT: Zhang, Zemin
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;	PRIOR APPLICATION NUMBER: 60/091982
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;	PRIOR FILING DATE: 1998-07-09

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RESULT 10

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; Sequence 23, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC25  
; CURRENT APPLICATION NUMBER: US/09/993,604  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1998-02-25  
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

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; Sequence 23, Application US/09989721  
; Patent No. US20020142961A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C55  
; CURRENT APPLICATION NUMBER: US/09/989,721  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;  
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RESULT 13  
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; Sequence 23, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
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; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C20  
; CURRENT APPLICATION NUMBER: US/09/992,598  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;  
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Desnoyers, Luc  
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APPLICANT: Zhang, Zemin  
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TITLE OF INVENTION: Acids Encoding the Same  
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PRIOR APPLICATION NUMBER: 60/090445



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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.le-127;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

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Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

Qy 121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL 180
Db 121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSSVL 180

Qy 181 HSGNFGTDLEQKHLWNPEDKGYVHLMITTAAEWSMSFFGFFFLTYIRDFOKISLRVEAN 240
Db 181 HSGNFGTDLEQKHLWNPEDKGYVHLMITTAAEWSMSFFGFFFLTYIRDFOKISLRVEAN 240

Qy 241 LHGLTLYDTAPCPINNERTRLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTRLLSRDI 266

RESULT 15
US-09-989-735-23

; Sequence 23, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
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; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1392; DB 3; Length 266;

Best Local Similarity 100.0%; Pred. No. 5.1e-127;

Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWFFQOGLSFLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Db 1 MWFFQOGLSFLPSALVITWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Qy 61 NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

Db 61 NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120

Qy 121 HVSGAVLTFMGMSLYNFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCCSVL 180

Db 121 HVSGAVLTFMGMSLYNFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCCSVL 180

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Db 181 HSGNFGTDLEQKLNHNPEKGYVLHMITTAAEWSMSFSFGFFLTYYIRDFQKISLRVEAN 240  
Qy 241 LHGLTLYDTAPCPINNERTRLLSRDI 266  
Db 241 LHGLTLYDTAPCPINNERTRLLSRDI 266

Search completed: August 28, 2006, 17:41:27  
Job time : 209 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: August 28, 2006, 17:32:09 ; Search time 41 Seconds  
(without alignments)  
624.236 Million cell updates/sec

Title: US-10-006-867-2  
Perfect score: 1392  
Sequence: 1 MMWFQQLSFLPSALVIWTS.....YDTAPCPINNERFLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	361.5	26.0	246	2 T13747	hypothetical prote
2	288	20.7	271	2 T19654	hypothetical prote
3	120	8.6	547	2 C88456	protein W03A5.2 li
4	103	7.4	332	2 E69312	nitrate reductase
5	98.5	7.1	1120	2 A10561	integral membrane
6	97	7.0	604	2 E72523	carbon starvation
7	96	6.9	495	2 S43882	NADH2 dehydrogenas
8	94	6.8	495	1 S16447	NADH2 dehydrogenas
9	93.5	6.7	379	2 D96506	hypothetical prote
10	93.5	6.7	429	2 F71651	putrescine-ornithi
11	93	6.7	1120	2 F90693	mechanosensitive c
12	93	6.7	1120	2 B85544	mechanosensitive c
13	93	6.7	1120	2 H64776	probable membrane
14	92.5	6.6	473	2 AE0801	probable amino aci
15	91.5	6.6	373	2 T24487	hypothetical prote
16	91.5	6.6	712	2 T02479	potassium transpor
17	90.5	6.5	614	2 E86194	hypothetical prote
18	90	6.5	400	2 C82503	hypothetical prote
19	90	6.5	492	2 S59107	NADH2 dehydrogenas
20	90	6.5	528	2 S19366	hypothetical prote
21	89.5	6.4	440	2 B64090	dicarboxylate tran
22	89.5	6.4	443	2 AE1706	hypothetical prote
23	89.5	6.4	495	2 G71019	hypothetical prote
24	89.5	6.4	599	2 T24333	hypothetical prote
25	89	6.4	428	2 A10034	probable transmemb
26	89	6.4	757	2 T42693	hypothetical prote
27	88.5	6.4	430	2 E75217	transporter PAB217
28	88.5	6.4	844	2 T23656	hypothetical prote
29	88	6.3	1165	2 A46180	adenylyl cyclase t

30	87.5	6.3	233	2 E70114	hemolysin III (ypl
31	87.5	6.3	429	2 D82181	GGDEF family prote
32	87.5	6.3	482	2 B69803	metabolite transpo
33	87.5	6.3	540	2 T24675	hypothetical prote
34	87	6.2	396	2 B91013	bicyclomycin resis
35	87	6.2	396	2 D85857	bicyclomycin resis
36	87	6.2	435	2 C95975	probable polysacch
37	87	6.2	613	2 C83496	glutathione-regula
38	86.5	6.2	400	2 C69757	transporter homolo
39	86.5	6.2	583	2 AH1151	glycerophosphoryl
40	86.5	6.2	770	2 G72589	hypothetical prote
41	86	6.2	373	2 D89865	hypothetical prote
42	86	6.2	389	2 G75133	hypothetical prote
43	86	6.2	396	1 E64987	bicyclomycin resis
44	86	6.2	703	2 E86146	F22L4.12 protein -
45	85.5	6.1	295	2 E81179	spermidine/putresc
46	85.5	6.1	296	2 AB0210	probable ABC sugar
47	85.5	6.1	498	2 S78184	NADH2 dehydrogenas
48	85	6.1	338	2 G70584	phosphate transpor
49	85	6.1	443	2 B86849	polysaccharide bios
50	85	6.1	1180	2 A47202	adenylate cyclase
51	84.5	6.1	457	2 T46332	hypothetical prote
52	84.5	6.1	463	2 AH0189	Amino acid permeas
53	84.5	6.1	479	2 D72354	lipopolysaccharide
54	84.5	6.1	491	2 T15605	hypothetical prote
55	84.5	6.1	638	2 T11801	NADH2 dehydrogenas
56	84.5	6.1	765	2 T22800	hypothetical prote
57	84	6.0	318	2 E95218	iron-compound ABC
58	84	6.0	460	2 A71028	hypothetical prote
59	84	6.0	575	2 B83586	probable permease
60	84	6.0	597	2 H82328	hypothetical prote
61	83.5	6.0	261	2 D64166	hypothetical prote
62	83.5	6.0	295	2 A81927	probable polyamine
63	83.5	6.0	521	2 T41621	hypothetical prote
64	83.5	6.0	638	2 B34285	NADH2 dehydrogenas
65	83	6.0	305	2 AD1998	hypothetical prote
66	83	6.0	318	2 C98082	hypothetical prote
67	83	6.0	427	2 F97790	putrescine-ornithi
68	83	6.0	460	2 D75106	hypothetical prote
69	83	6.0	496	2 B83503	probable amino aci
70	83	6.0	637	2 S01509	NADH2 dehydrogenas
71	82.5	5.9	391	2 S48967	ethanolaminephosph
72	82.5	5.9	418	2 E83175	probable aromatic
73	82.5	5.9	452	2 A71877	proline/betaine tr
74	82.5	5.9	494	2 T14246	NADH2 dehydrogenas
75	82.5	5.9	596	2 S46001	probable amino aci
76	82	5.9	317	2 D84098	hypothetical prote
77	82	5.9	327	2 A82241	probable ABC trans
78	82	5.9	356	2 D86408	purine permease li
79	82	5.9	446	2 A38244	citrate transport
80	82	5.9	461	2 H64636	proline/betaine tr
81	82	5.9	548	2 B87423	cytochrome-c oxida
82	82	5.9	557	2 T41588	probable amino-aci
83	82	5.9	573	2 T23589	hypothetical prote
84	82	5.9	693	2 T19598	hypothetical prote
85	82	5.9	1139	2 A10379	probable potassium
86	81.5	5.9	205	2 D95200	conserved hypothet
87	81.5	5.9	205	2 C98067	hypothetical prote
88	81.5	5.9	292	2 AE1539	sugar ABC transpor
89	81.5	5.9	307	2 H97018	bacitracin resista
90	81.5	5.9	351	2 C86408	F3H9.12 protein -
91	81.5	5.9	438	2 B83017	probable MFS trans
92	81.5	5.9	485	2 T24677	hypothetical prote
93	81.5	5.9	486	2 S51503	NADH2 dehydrogenas
94	81.5	5.9	734	2 T13785	NADH2 dehydrogenas
95	81	5.8	293	2 C95892	probable glycerol-
96	81	5.8	293	2 D71517	probable metal tra
97	81	5.8	438	2 H85822	probable transport
98	81	5.8	479	2 C64878	probable amino aci
99	81	5.8	479	2 T44326	hypothetical prote
100	81	5.8	487	2 E96782	hypothetical prote
101	81	5.8	544	2 T24633	hypothetical prote
102	81	5.8	710	2 T12143	NADH2 dehydrogenas



103	80.5	5.8	359	2	F90055	conserved hypothet	176	77.5	5.6	363	2	A72771	hypothetical prote
104	80.5	5.8	385	2	T07130	probable amino aci	177	77.5	5.6	461	2	H85755	probable amino aci
105	80.5	5.8	433	2	AC0043	anaerobic C4-dicar	178	77.5	5.6	464	2	C83605	probable transport
106	80.5	5.8	473	2	G69789	sugar transporter	179	77.5	5.6	479	2	A90863	probable amino aci
107	80.5	5.8	528	2	E81186	L-lactate permease	180	77.5	5.6	499	2	AG0882	probable amino aci
108	80.5	5.8	590	1	QRBYPR	arginine transport	181	77.5	5.6	506	2	F64862	hypothetical prote
109	80.5	5.8	637	2	S78171	heme lyase yejR -	182	77.5	5.6	510	2	D96741	hypothetical prote
110	80.5	5.8	728	2	T13794	NADH2 dehydrogenas	183	77.5	5.6	510	2	E71695	hypothetical prote
111	80	5.7	266	2	G83178	conserved hypothet	184	77.5	5.6	513	2	A82432	sodium/solute symp
112	80	5.7	291	2	A97387	hypothetical prote	185	77.5	5.6	526	2	T01853	probable hexose tr
113	80	5.7	291	2	AB2605	hypothetical prote	186	77.5	5.6	532	1	S49345	cytochrome-c oxida
114	80	5.7	429	1	C41903	arsenical pump mem	187	77.5	5.6	535	2	S76103	hypothetical prote
115	80	5.7	702	2	T12141	NADH2 dehydrogenas	188	77.5	5.6	649	2	A69478	NADH2 dehydrogenas
116	80	5.7	902	2	C83964	cation-transportin	189	77.5	5.6	717	2	T46172	phenylalanine ammo
117	80	5.7	1123	2	T48586	hypothetical prote	190	77.5	5.6	1118	2	B83018	conserved hypothet
118	79.5	5.7	323	2	T32279	hypothetical prote	191	77	5.5	282	2	AD1231	B. subtilis YxkD p
119	79.5	5.7	405	2	T42992	cyclin D - Caenorh	192	77	5.5	332	2	D95973	probable sugar upt
120	79.5	5.7	445	2	S77010	nickel resistance	193	77	5.5	417	2	F90270	amino acid permeas
121	79.5	5.7	499	2	F75059	NADH-dehydrogenase	194	77	5.5	438	2	G64962	shikimate transpor
122	79.5	5.7	539	1	S49495	cytochrome-c oxida	195	77	5.5	438	2	B69855	amino acid permeas
123	79.5	5.7	542	2	AG3605	potassium efflux s	196	77	5.5	471	2	H90502	phosphate transpor
124	79.5	5.7	570	2	AH2765	cytochrome c oxida	197	77	5.5	519	2	JQ0124	membrane protein S
125	79.5	5.7	598	2	E97546	cytochrome c oxida	198	77	5.5	551	1	A55582	cytochrome-c oxida
126	79.5	5.7	741	2	T13051	NADH2 dehydrogenas	199	77	5.5	579	2	AB2177	hypothetical prote
127	79.5	5.7	831	2	B40204	Na+/H+-exchanging	200	77	5.5	662	2	H84984	bo-type ubiquinol
128	79	5.7	172	2	S55015	NADH2 dehydrogenas	201	77	5.5	710	2	T20635	hypothetical prote
129	79	5.7	183	2	A64009	hypothetical prote	202	77	5.5	739	2	T13038	NADH2 dehydrogenas
130	79	5.7	281	2	T26244	hypothetical prote	203	77	5.5	749	2	E71275	hypothetical integ
131	79	5.7	293	2	B83783	hypothetical prote	204	77	5.5	915	2	H96709	hypothetical prote
132	79	5.7	293	2	H72064	ABC transporter, p	205	77	5.5	936	2	T26521	hypothetical prote
133	79	5.7	293	2	C86558	metal transport pr	206	76.5	5.5	152	2	C72681	hypothetical prote
134	79	5.7	307	2	C81862	conserved hypothet	207	76.5	5.5	269	2	H69768	conserved hypothet
135	79	5.7	377	2	T49063	nodulin-like prote	208	76.5	5.5	284	2	G64052	probable formate t
136	79	5.7	390	2	H72265	hypothetical prote	209	76.5	5.5	289	2	T02095	transmembrane prot
137	79	5.7	395	2	D69312	molybdopterin oxid	210	76.5	5.5	300	2	S40858	hypothetical 32.9K
138	79	5.7	410	2	E84998	hypothetical prote	211	76.5	5.5	300	2	H91233	probable transport
139	79	5.7	438	2	B90976	shikimate transpor	212	76.5	5.5	300	2	H86080	probable transport
140	79	5.7	444	2	G82392	conserved hypothet	213	76.5	5.5	301	2	B82235	conserved hypothet
141	79	5.7	453	2	AF1198	conserved hypothet	214	76.5	5.5	301	2	T27585	hypothetical prote
142	79	5.7	473	2	T31717	hypothetical prote	215	76.5	5.5	305	2	D83699	hypothetical prote
143	79	5.7	489	2	B97289	lysine-specific pe	216	76.5	5.5	334	2	A75142	oligopeptide trans
144	79	5.7	685	2	T12139	NADH2 dehydrogenas	217	76.5	5.5	370	2	AB3334	daunorubicin resis
145	79	5.7	819	2	G69801	hypothetical prote	218	76.5	5.5	377	2	C89456	protein F55A4.8 [i
146	79	5.7	2198	2	T20371	hypothetical prote	219	76.5	5.5	382	2	B82177	Na+/H+ antiporter
147	78.5	5.6	169	2	H84191	hypothetical prote	220	76.5	5.5	395	2	AD0678	probable membrane
148	78.5	5.6	241	2	S00836	hypothetical prote	221	76.5	5.5	431	2	H84069	hypothetical prote
149	78.5	5.6	366	2	C64449	mcBE protein - Bsc	222	76.5	5.5	474	2	F64119	NAD(P) transhydrog
150	78.5	5.6	405	2	T26678	cationic amino aci	223	76.5	5.5	475	2	E69643	histidine permease
151	78.5	5.6	412	2	G89773	hypothetical prote	224	76.5	5.5	495	2	AD0402	glycerol kinase (E
152	78.5	5.6	493	2	F75113	NADH dehydrogenase	225	76.5	5.5	548	2	B72542	probable cytochrom
153	78.5	5.6	579	2	A70954	hypothetical prote	226	76.5	5.5	725	2	S64124	probable membrane
154	78.5	5.6	622	2	E69609	cytochrome-c oxida	227	76.5	5.5	746	2	T13698	NADH2 dehydrogenas
155	78.5	5.6	624	2	T48587	peptide transporte	228	76.5	5.5	855	2	T47534	hypothetical prote
156	78.5	5.6	732	2	T13814	NADH2 dehydrogenas	229	76.5	5.5	1187	2	T20544	hypothetical prote
157	78.5	5.6	744	2	T13485	NADH2 dehydrogenas	230	76.5	5.5	1342	2	E85614	cell division prot
158	78.5	5.6	1325	2	T01037	hypothetical prote	231	76.5	5.5	1342	2	G90750	cell division prot
159	78	5.6	158	2	T26519	hypothetical prote	232	76	5.5	261	2	A64066	probable membrane
160	78	5.6	307	2	D81082	conserved hypothet	233	76	5.5	275	2	C97028	probable metal-bin
161	78	5.6	335	2	E81736	phospho-N-acetylm	234	76	5.5	281	2	AB1585	B. subtilis YxkD p
162	78	5.6	382	2	E97742	hypothetical prote	235	76	5.5	282	2	D97767	hypothetical prote
163	78	5.6	388	2	G75375	hypothetical prote	236	76	5.5	336	2	T23902	hypothetical prote
164	78	5.6	396	2	AF0785	bicyclomycin resis	237	76	5.5	365	2	F82210	amino acid ABC tra
165	78	5.6	414	2	S53075	probable membrane	238	76	5.5	415	2	G83568	probable permease
166	78	5.6	422	2	H64489	hypothetical prote	239	76	5.5	447	2	C84306	hypothetical prote
167	78	5.6	462	2	T48661	acetate-CoA ligase	240	76	5.5	452	2	S46037	prephenate dehydro
168	78	5.6	688	2	T06299	potassium transpor	241	76	5.5	480	2	G83414	cytochrome-c oxida
169	78	5.6	701	2	T15238	hypothetical prote	242	76	5.5	502	2	JN0113	nicotinic acetylch
170	77.5	5.6	212	2	E83936	hypothetical prote	243	76	5.5	558	2	S08270	cytochrome-c oxida
171	77.5	5.6	283	2	H95887	probable ABC trans	244	76	5.5	578	2	T13664	NADH2 dehydrogenas
172	77.5	5.6	292	2	AD1182	sugar ABC transpor	245	76	5.5	617	2	T20409	hypothetical prote
173	77.5	5.6	293	2	AH0143	probable membrane	246	76	5.5	659	2	E85889	probable oxidoredu
174	77.5	5.6	296	2	C95326	AttA2-like ABC tra	247	76	5.5	659	2	B91045	probable oxidoredu
175	77.5	5.6	335	2	A72289	oligopeptide ABC t	248	76	5.5	669	1	DNMUU5	NADH2 dehydrogenas

249	76	5.5	956	2	A89153	protein C24B5.3 [i
250	76	5.5	958	2	AC0204	probable integral
251	76	5.5	966	2	H97717	hypothetical prote
252	76	5.5	971	2	H71719	hypothetical prote
253	76	5.5	1052	2	T50127	hypothetical prote
254	76	5.5	1074	2	T45094	probable arabinosy
255	76	5.5	1166	2	A49201	adenylate cyclase
256	75.5	5.4	210	2	T01623	hypothetical prote
257	75.5	5.4	237	2	A99737	hypothetical prote
258	75.5	5.4	237	2	B85587	hypothetical prote
259	75.5	5.4	240	2	D71939	hypothetical prote
260	75.5	5.4	252	2	B47188	MHC class II histo
261	75.5	5.4	295	1	QOSABT	hypothetical prote
262	75.5	5.4	296	2	E83049	conserved hypothet
263	75.5	5.4	297	2	AE0400	probable membrane
264	75.5	5.4	322	2	A12880	ABC transporter, m
265	75.5	5.4	322	2	A97657	ferrichrome ABC tr
266	75.5	5.4	338	2	C83785	ferrichrome ABC tr
267	75.5	5.4	397	2	D69538	arsenite transport
268	75.5	5.4	432	2	A42476	hypothetical prote
269	75.5	5.4	432	2	AD0766	probable O-antigen
270	75.5	5.4	441	2	B71027	probable nfeD prot
271	75.5	5.4	454	2	E85826	probable amino aci
272	75.5	5.4	454	2	H90980	probable amino aci
273	75.5	5.4	454	2	E64966	probable amino aci
274	75.5	5.4	454	2	AG0763	probable amino aci
275	75.5	5.4	459	2	S42238	tetracyclin resist
276	75.5	5.4	476	2	S23576	melibiose transpor
277	75.5	5.4	492	2	AC0768	probable transmemb
278	75.5	5.4	513	2	I39534	hypothetical prote
279	75.5	5.4	532	2	D95287	conserved hypothet
280	75.5	5.4	567	2	B81408	probable thiol-dis
281	75.5	5.4	676	1	S54750	cytochrome c-type
282	75.5	5.4	735	2	F84726	probable Na+/H+ an
283	75.5	5.4	740	2	T12223	NADH2 dehydrogenas
284	75.5	5.4	832	2	A40205	Na+/H+-exchanging
285	75.5	5.4	914	2	I40529	penicillin-binding
286	75.5	5.4	932	2	T25941	hypothetical prote
287	75	5.4	262	2	B83827	hypothetical prote
288	75	5.4	289	2	T12037	probable aquaporin
289	75	5.4	291	2	T04139	transmembrane prot
290	75	5.4	298	2	S75972	hypothetical prote
291	75	5.4	322	2	B98193	sugar ABC transpor
292	75	5.4	322	2	AH3093	hypothetical prote
293	75	5.4	395	2	S73531	CDP-diglyceride sy
294	75	5.4	398	2	B71193	hypothetical prote
295	75	5.4	429	1	B41902	arsenical pump mem
296	75	5.4	432	2	H71092	hypothetical prote
297	75	5.4	451	2	E90171	inorganic phosphat
298	75	5.4	461	2	AF1179	hexose phosphate t
299	75	5.4	494	2	A82294	probable carbon st
300	75	5.4	507	2	AI1739	amino acid antipor
301	75	5.4	559	2	T33168	hypothetical prote
302	75	5.4	599	2	T48383	uracil transporter
303	75	5.4	625	2	D45335	cytochrome-c oxida
304	75	5.4	643	2	E69373	conserved hypothet
305	75	5.4	917	2	I49699	glycoprotein i30 -
306	75	5.4	1056	2	G84865	hypothetical prote
307	75	5.4	1294	2	S77690	probable membrane
308	74.5	5.4	174	2	F90494	conserved hypothet
309	74.5	5.4	288	2	T09794	major intrinsic pr
310	74.5	5.4	293	2	A96209	motC protein [impo
311	74.5	5.4	293	2	AH3077	hypothetical prote
312	74.5	5.4	305	2	B33465	lic-1 protein B -
313	74.5	5.4	311	2	F70184	ribose/galactose A
314	74.5	5.4	323	2	T31697	hypothetical prote
315	74.5	5.4	324	1	C47691	phospho-N-acetylmu
316	74.5	5.4	325	2	F82558	lipopolysaccharide
317	74.5	5.4	366	2	H86614	Cr838 hypothetical
318	74.5	5.4	366	2	C72009	conserved hypothet
319	74.5	5.4	367	2	T13813	NADH2 dehydrogenas
320	74.5	5.4	399	2	T27853	hypothetical prote
321	74.5	5.4	409	1	F69814	fosmidmycin resist

322	74.5	5.4	411	2	T03836	phosphate/phosphoe
323	74.5	5.4	439	2	AB0389	branched-chain ami
324	74.5	5.4	447	2	T19112	hypothetical prote
325	74.5	5.4	469	1	BDEC	melibiose carrier
326	74.5	5.4	469	2	C86107	melibiose permease
327	74.5	5.4	469	2	F91266	melibiose permease
328	74.5	5.4	476	2	AG0502	probable amino-aci
329	74.5	5.4	544	2	T32895	hypothetical prote
330	74.5	5.4	560	2	T32727	hypothetical prote
331	74.5	5.4	726	2	T12215	NADH2 dehydrogenas
332	74.5	5.4	889	2	AD2215	two-component hybr
333	74.5	5.4	953	2	S19427	probable membrane
334	74	5.3	277	2	E72030	conserved hypothet
335	74	5.3	277	2	A86594	CT560 hypothetical
336	74	5.3	281	2	H90387	hypothetical prote
337	74	5.3	296	2	C69635	transcription repr
338	74	5.3	303	2	T25501	hypothetical prote
339	74	5.3	322	1	A29928	membrane-associate
340	74	5.3	370	2	H84351	hypothetical prote
341	74	5.3	380	2	S34964	rfc protein - Shig
342	74	5.3	400	2	F86887	hypothetical prote
343	74	5.3	401	2	E82951	probable MFS trans
344	74	5.3	404	2	A36865	ammonium transport
345	74	5.3	407	2	G81010	conserved hypothet
346	74	5.3	425	2	H71554	hypothetical prote
347	74	5.3	431	2	T41614	malate permease -
348	74	5.3	437	2	G82032	probable permease
349	74	5.3	446	2	A42661	citrate carrier pr
350	74	5.3	446	2	AD0509	citrate-sodium sym
351	74	5.3	446	2	B42661	citrate carrier pr
352	74	5.3	459	2	T11084	NADH2 dehydrogenas
353	74	5.3	473	2	AG0948	probable membrane
354	74	5.3	508	2	A83839	hypothetical prote
355	74	5.3	530	2	F85768	PTS system, maltos
356	74	5.3	530	2	A99920	PTS system, maltos
357	74	5.3	532	2	H96840	hypothetical prote
358	74	5.3	542	2	F90457	hypothetical prote
359	74	5.3	592	2	T25837	hypothetical prote
360	74	5.3	612	2	C90419	glucan 1,4 alpha g
361	74	5.3	740	2	AH0600	probable membrane
362	74	5.3	817	2	T51787	hypothetical prote
363	74	5.3	908	2	S51293	probable membrane
364	74	5.3	947	2	H85088	hypothetical prote
365	73.5	5.3	218	1	D69372	osmoprotection pro
366	73.5	5.3	240	2	A64652	hypothetical prote
367	73.5	5.3	299	2	B83323	hypothetical prote
368	73.5	5.3	329	2	AD0442	probable branched-
369	73.5	5.3	337	2	T23942	hypothetical prote
370	73.5	5.3	343	2	G86709	hypothetical prote
371	73.5	5.3	363	2	AF2457	hypothetical prote
372	73.5	5.3	372	2	A98157	probable permease
373	73.5	5.3	372	2	AH3130	ABC transporter, m
374	73.5	5.3	391	2	S30046	potassium channel
375	73.5	5.3	409	2	T03718	suppressor 2 prote
376	73.5	5.3	423	2	C81266	probable efflux pr
377	73.5	5.3	425	2	C65100	hypothetical 46.6
378	73.5	5.3	426	2	F72049	phosphate permease
379	73.5	5.3	443	2	F85972	probable transport
380	73.5	5.3	443	2	G91127	probable transport
381	73.5	5.3	463	2	F90285	metabolite transpo
382	73.5	5.3	476	2	AC1023	melibiose carrier
383	73.5	5.3	477	2	F82200	cytochrome-c oxida
384	73.5	5.3	498	2	F89861	Na+/H+-antipoter
385	73.5	5.3	507	2	B97765	ADP,ATP carrier pr
386	73.5	5.3	522	2	D86263	F13K23.21 protein
387	73.5	5.3	526	2	S74025	conserved hypothet
388	73.5	5.3	526	2	T29433	hypothetical prote
389	73.5	5.3	547	2	AB2639	pH adaption potass
390	73.5	5.3	548	2	C97421	phaD protein (X933
391	73.5	5.3	592	2	E75032	carbon starvation
392	73.5	5.3	607	2	S19585	serotonin transpor
393	73.5	5.3	607	2	S63395	probable membrane
394	73.5	5.3	630	2	S30604	neurotransmitter t

395	73.5	5.3	674	2	E82954	conserved hypothet	468	72.5	5.2	741	2	T13085	NADH2 dehydrogenas
396	73.5	5.3	699	2	T13730	NADH2 dehydrogenas	469	72.5	5.2	743	2	T13073	NADH2 dehydrogenas
397	73.5	5.3	875	2	H90371	proteinase [import	470	72.5	5.2	744	2	T13040	NADH2 dehydrogenas
398	73.5	5.3	885	2	B69783	transporter homolo	471	72.5	5.2	744	2	T13757	NADH2 dehydrogenas
399	73.5	5.3	889	2	T20123	hypothetical prote	472	72.5	5.2	917	2	T17244	hypothetical prote
400	73.5	5.3	1099	2	A55405	adenylate cyclase	473	72.5	5.2	923	2	C97487	conserved hypothet
401	73.5	5.3	1128	2	T04922	hypothetical prote	474	72.5	5.2	923	2	AC2705	probable membrane
402	73.5	5.3	1343	2	AF0611	cell division prot	475	72.5	5.2	953	2	S54478	probable mmp11 pro
403	73.5	5.3	2818	2	B55282	neurofibromatosis-	476	72.5	5.2	958	2	A70634	mitochondrial Cl-t
404	73.5	5.3	2820	2	JC5196	neurofibromin I -	477	72.5	5.2	978	2	JC8067	NADH dehydrogenase
405	73.5	5.3	2825	2	I54352	neurofibromin - mo	478	72.5	5.2	1148	2	H90175	cell division prot
406	73	5.2	140	2	C83199	hypothetical prote	479	72.5	5.2	1329	2	A64828	protein T23G18.2 [
407	73	5.2	193	2	B91170	hypothetical membr	480	72.5	5.2	2658	2	A86216	hypothetical prote
408	73	5.2	193	2	B86016	hypothetical prote	481	72	5.2	215	2	F75166	membrane protein -
409	73	5.2	261	2	AC0251	high-affinity zinc	482	72	5.2	242	2	S49598	hypothetical prote
410	73	5.2	262	2	F97151	ABC transported MD	483	72	5.2	249	2	A71234	hypothetical prote
411	73	5.2	282	2	H71696	hypothetical prote	484	72	5.2	252	2	A71165	probable dimethyl
412	73	5.2	283	2	D83009	probable permease	485	72	5.2	257	2	AC1024	FP0 protein - fowl
413	73	5.2	292	2	C95147	licB protein [impo	486	72	5.2	260	1	WMV2P0	probable membrane
414	73	5.2	294	2	D81434	probable 4-hydroxy	487	72	5.2	261	2	S62047	hypothetical prote
415	73	5.2	296	2	A98015	hypothetical prote	488	72	5.2	282	2	D98058	hypothetical prote
416	73	5.2	301	2	AH2064	hypothetical prote	489	72	5.2	286	2	T23066	hypothetical prote
417	73	5.2	311	2	T33436	hypothetical prote	490	72	5.2	315	2	B83778	ferrichrome ABC tr
418	73	5.2	364	2	D95959	hypothetical prote	491	72	5.2	339	2	E86761	conserved hypothet
419	73	5.2	384	2	S37608	conserved hypothet	492	72	5.2	339	2	T23244	hypothetical prote
420	73	5.2	399	2	AE0396	NADH2 dehydrogenas	493	72	5.2	355	2	A55733	G protein-coupled
421	73	5.2	401	2	T49929	probable sugar tra	494	72	5.2	359	2	AF3044	hypothetical prote
422	73	5.2	436	2	S77639	exopolysaccharide	495	72	5.2	361	2	C84246	ribose ABC transpo
423	73	5.2	437	2	D86633	amino acid permeas	496	72	5.2	367	2	C82943	ferrichrome ABC tr
424	73	5.2	453	2	AD1556	conserved hypothet	497	72	5.2	374	2	F98241	mtlK protein (AF00
425	73	5.2	456	2	H97735	hypothetical prote	498	72	5.2	378	2	T34372	hypothetical prote
426	73	5.2	470	2	B86118	transport of D-ala	499	72	5.2	417	2	F90916	probable transport
427	73	5.2	470	2	B91277	D-serine/D-alanine	500	72	5.2	417	2	F64915	membrane protein y
428	73	5.2	470	2	S56433	D-serine/D-alanine	501	72	5.2	417	2	C85765	probable transport
429	73	5.2	495	1	S25942	NADH2 dehydrogenas	502	72	5.2	421	2	B84129	ammonium transport
430	73	5.2	507	2	AB1370	amino acid antipor	503	72	5.2	431	2	C82432	sugar transporter
431	73	5.2	574	2	T05964	probable low-affin	504	72	5.2	440	2	C82410	conserved hypothet
432	73	5.2	633	2	T19189	hypothetical prote	505	72	5.2	440	2	C75107	nodulation protein
433	73	5.2	639	2	G88839	protein C10C6.5 [i	506	72	5.2	444	2	T24076	hypothetical prote
434	73	5.2	700	2	T13668	NADH2 dehydrogenas	507	72	5.2	447	2	AE0094	probable gluconate
435	73	5.2	732	2	T14233	NADH2 dehydrogenas	508	72	5.2	453	2	H71732	cytochrome D ubiqu
436	73	5.2	1564	2	T27121	hypothetical prote	509	72	5.2	463	2	H69822	sodium-glutamate s
437	73	5.2	3079	1	RGBYI2	probable GTPase-ac	510	72	5.2	482	2	T17022	NADH2 dehydrogenas
438	73	5.2	3898	1	GNWVHB	genome polyprotein	511	72	5.2	507	2	B71695	adp, ATP carrier p
439	72.5	5.2	118	2	G64394	hypothetical prote	512	72	5.2	524	2	AD1897	hypothetical prote
440	72.5	5.2	235	2	F95230	membrane protein (	513	72	5.2	530	1	G64918	phosphotransferase
441	72.5	5.2	235	2	A99095	conserved hypothet	514	72	5.2	530	2	T51836	high affinity nitr
442	72.5	5.2	235	2	AF0598	probable membrane	515	72	5.2	582	2	H96604	probable 3'-5', exo
443	72.5	5.2	271	2	T11704	NADH2 dehydrogenas	516	72	5.2	602	2	AC2313	hypothetical prote
444	72.5	5.2	284	2	AH0680	probable dimethyl	517	72	5.2	608	2	S76192	hypothetical prote
445	72.5	5.2	286	2	B99213	cytochrome C oxida	518	72	5.2	614	2	T13727	NADH2 dehydrogenas
446	72.5	5.2	297	2	F82039	ribonuclease BN VC	519	72	5.2	620	2	F83976	cytochrome-c oxida
447	72.5	5.2	308	2	AF0461	probable membrane	520	72	5.2	628	2	AG2707	hypothetical tran
448	72.5	5.2	330	2	D95902	probable sugar ABC	521	72	5.2	629	2	H97489	hypothetical prote
449	72.5	5.2	347	2	AD2201	hypothetical prote	522	72	5.2	641	2	AG2164	transporter, trunc
450	72.5	5.2	368	2	T13815	NADH2 dehydrogenas	523	72	5.2	644	2	B97885	NADH2 dehydrogenas
451	72.5	5.2	375	2	B40205	Na+/H+-exchanging	524	72	5.2	681	2	T13566	NADH2 dehydrogenas
452	72.5	5.2	421	2	T22969	hypothetical prote	525	72	5.2	689	2	T11917	hypothetical prote
453	72.5	5.2	434	2	D65132	hypothetical 46.5	526	72	5.2	692	2	T33786	NADH2 dehydrogenas
454	72.5	5.2	458	2	B90623	NADH dehydrogenase	527	72	5.2	696	2	T12160	NADH2 dehydrogenas
455	72.5	5.2	459	2	T19110	hypothetical prote	528	72	5.2	698	2	T12565	NADH2 dehydrogenas
456	72.5	5.2	461	2	G85059	probable sugar tra	529	72	5.2	700	2	T13763	NADH2 dehydrogenas
457	72.5	5.2	461	2	S75711	hypothetical prote	530	72	5.2	719	2	T13793	NADH2 dehydrogenas
458	72.5	5.2	491	2	H83979	lysine decarboxyla	531	72	5.2	796	2	S62464	conserved hypothet
459	72.5	5.2	494	1	F69355	Na+/H+ antipoter	532	72	5.2	906	2	S35312	coatomer complex b
460	72.5	5.2	498	2	B89832	hypothetical prote	533	72	5.2	2150	2	T08165	RNA1 polyprotein -
461	72.5	5.2	523	2	A11970	hypothetical prote	534	72	5.2	2150	2	T08165	hypothetical prote
462	72.5	5.2	615	2	S77084	ABC-type transporter	535	71.5	5.1	213	2	A71049	hypothetical prote
463	72.5	5.2	646	2	B70001	ABC transporter (p	536	71.5	5.1	232	2	E86825	hypothetical prote
464	72.5	5.2	682	2	T12715	NADH2 dehydrogenas	537	71.5	5.1	260	2	H89899	phosphatidate cyti
465	72.5	5.2	684	2	T13491	NADH2 dehydrogenas	538	71.5	5.1	281	2	A55862	aarA protein - Pro
466	72.5	5.2	704	2	T13665	NADH2 dehydrogenas	539	71.5	5.1	283	2	B69769	hypothetical prote
467	72.5	5.2	736	2	T12716	NADH2 dehydrogenas	540	71.5	5.1	285	2	AI1127	Staphylococcus xyl

541	71.5	5.1	295	2	AB0462	sn-glycerol-3-phos	614	71	5.1	468	2	D83625	probable transport
542	71.5	5.1	303	2	T32277	hypothetical prote	615	71	5.1	469	2	E86075	probable permease
543	71.5	5.1	308	2	H70767	hypothetical prote	616	71	5.1	478	2	A97079	MDR-type permease
544	71.5	5.1	323	2	G84003	DNA transport mach	617	71	5.1	492	2	D75188	proline symporter
545	71.5	5.1	324	2	F81018	iron(III) ABC tran	618	71	5.1	498	2	H81796	NADH2 dehydrogenas
546	71.5	5.1	337	2	F82214	galactoside ABC tr	619	71	5.1	502	1	ACHUA7	nicotinic acetylch
547	71.5	5.1	341	2	F82712	integral membrane	620	71	5.1	502	2	G02259	alpha 7 neuronal n
548	71.5	5.1	348	2	A82322	octaprenyl-diphosp	621	71	5.1	502	2	A57175	nicotinic receptor
549	71.5	5.1	349	2	T31856	hypothetical prote	622	71	5.1	502	2	T01378	nicotinic acetylch
550	71.5	5.1	373	2	A98094	type III secretion	623	71	5.1	509	2	A82840	beta-lactamase ind
551	71.5	5.1	373	2	E85939	hypothetical prote	624	71	5.1	541	2	D82302	iron(III) ABC tran
552	71.5	5.1	373	2	D71142	hypothetical prote	625	71	5.1	555	2	T24671	hypothetical prote
553	71.5	5.1	382	2	H85014	probable acetyltra	626	71	5.1	569	2	T00477	probable amino aci
554	71.5	5.1	391	2	A55119	potassium channel	627	71	5.1	579	2	AB1414	ABC transporter (A
555	71.5	5.1	406	2	C86904	transporter yxbD [	628	71	5.1	593	2	AI0559	probable ABC trans
556	71.5	5.1	418	2	H97763	proline/betaine tr	629	71	5.1	594	2	A49804	cellular Hsp70 hom
557	71.5	5.1	432	2	D95369	conserved hypothet	630	71	5.1	612	2	S74936	sulfur deprivation
558	71.5	5.1	445	2	T20190	hypothetical prote	631	71	5.1	684	2	T12151	NADH2 dehydrogenas
559	71.5	5.1	470	2	A69751	histidine permease	632	71	5.1	685	2	T12138	NADH2 dehydrogenas
560	71.5	5.1	470	2	C70554	hypothetical prote	633	71	5.1	686	2	T12128	NADH2 dehydrogenas
561	71.5	5.1	477	2	F86670	lysine specific pe	634	71	5.1	688	2	T13237	NADH2 dehydrogenas
562	71.5	5.1	497	2	G81598	serine hydroxymeth	635	71	5.1	688	2	T13249	NADH2 dehydrogenas
563	71.5	5.1	506	2	F88954	protein K04F1.14 [	636	71	5.1	698	2	T12560	NADH2 dehydrogenas
564	71.5	5.1	512	2	S75887	hypothetical prote	637	71	5.1	699	2	T12648	NADH2 dehydrogenas
565	71.5	5.1	519	2	E86555	serine hydroxymeth	638	71	5.1	704	2	T13729	NADH2 dehydrogenas
566	71.5	5.1	519	2	H72067	glycine hydroxymet	639	71	5.1	737	2	T13067	NADH2 dehydrogenas
567	71.5	5.1	532	2	S59087	cytochrome-c oxida	640	71	5.1	918	2	A36337	membrane glycoprot
568	71.5	5.1	532	2	S66087	amino acid transpo	641	71	5.1	1506	2	T51900	related to PAN2 pr
569	71.5	5.1	533	2	H69326	conserved hypothet	642	70.5	5.1	133	2	AI3582	hypothetical prote
570	71.5	5.1	534	2	C87023	probable cell divi	643	70.5	5.1	167	2	T20548	hypothetical prote
571	71.5	5.1	539	2	S77595	cytochrome-c oxida	644	70.5	5.1	175	2	T39999	hypothetical prote
572	71.5	5.1	654	2	H89871	hypothetical prote	645	70.5	5.1	210	2	F64609	conserved hypothet
573	71.5	5.1	663	2	AG2696	cytochrome c-type	646	70.5	5.1	214	2	S76538	hypothetical prote
574	71.5	5.1	663	2	G97478	cytochrome c-type	647	70.5	5.1	237	2	C64815	ybhM protein - Esc
575	71.5	5.1	665	2	B96668	probable acyl-CoA	648	70.5	5.1	253	2	F75067	hypothetical prote
576	71.5	5.1	672	2	AF3084	conserved hypothet	649	70.5	5.1	263	2	T29414	hypothetical prote
577	71.5	5.1	672	2	C98202	hypothetical prote	650	70.5	5.1	263	2	T04051	hypothetical prote
578	71.5	5.1	696	2	B87265	Kup system potassi	651	70.5	5.1	267	2	H72590	hypothetical prote
579	71.5	5.1	698	2	T12590	NADH2 dehydrogenas	652	70.5	5.1	285	2	T12435	probable plasma me
580	71.5	5.1	718	1	B64040	hypothetical prote	653	70.5	5.1	285	2	D87209	probable transmemb
581	71.5	5.1	730	2	T12224	NADH2 dehydrogenas	654	70.5	5.1	286	2	T02451	plasma membrane in
582	71.5	5.1	741	2	T12642	NADH2 dehydrogenas	655	70.5	5.1	288	2	S41194	transmembrane prot
583	71.5	5.1	741	2	T12701	NADH2 dehydrogenas	656	70.5	5.1	290	2	A69779	conserved hypothet
584	71.5	5.1	746	2	T13678	NADH2 dehydrogenas	657	70.5	5.1	297	2	G69357	hypothetical prote
585	71.5	5.1	756	2	T04187	subtilisin-like pr	658	70.5	5.1	312	2	AB0306	probable membrane
586	71.5	5.1	765	2	F97186	probable cell wall	659	70.5	5.1	315	1	C69763	ferrichrome ABC tr
587	71.5	5.1	770	2	T23999	hypothetical prote	660	70.5	5.1	315	2	C81962	probable inner mem
588	71.5	5.1	854	2	D82324	conserved hypothet	661	70.5	5.1	318	2	E71054	probable sodium de
589	71.5	5.1	1067	2	AB0260	probable phage hos	662	70.5	5.1	327	2	D75196	hypothetical prote
590	71.5	5.1	1679	2	T50091	yeast Ecm29 cell w	663	70.5	5.1	346	2	AB0187	probable iron-side
591	71	5.1	200	1	F45456	NADH2 dehydrogenas	664	70.5	5.1	349	2	T33948	hypothetical prote
592	71	5.1	228	2	AE2541	hypothetical prote	665	70.5	5.1	358	2	T22823	hypothetical prote
593	71	5.1	229	2	A64137	molybdenum transpo	666	70.5	5.1	386	2	E69765	branched chain ami
594	71	5.1	243	2	B86740	lipopolysaccharide	667	70.5	5.1	387	2	AE1062	hypothetical prote
595	71	5.1	260	2	T30669	probable trans-act	668	70.5	5.1	394	2	C81333	probable efflux pu
596	71	5.1	260	2	C82116	flagellar biosynth	669	70.5	5.1	408	2	B42290	probable membrane
597	71	5.1	261	2	H69217	hypothetical prote	670	70.5	5.1	419	2	B90033	hypothetical prote
598	71	5.1	272	2	T11689	NADH2 dehydrogenas	671	70.5	5.1	430	2	A95935	conserved hypothet
599	71	5.1	297	2	AD2318	transcription regu	672	70.5	5.1	434	2	T15799	hypothetical prote
600	71	5.1	305	2	E90461	hypothetical prote	673	70.5	5.1	443	2	D71058	hypothetical prote
601	71	5.1	316	2	AB2931	hypothetical prote	674	70.5	5.1	446	2	B99284	hypothetical prote
602	71	5.1	316	2	D98351	dipeptide ABC tran	675	70.5	5.1	457	2	A83677	sodium-dependent t
603	71	5.1	333	2	T41669	hypothetical prote	676	70.5	5.1	458	2	B90615	NADH dehydrogenase
604	71	5.1	364	2	H83787	hypothetical prote	677	70.5	5.1	474	2	T38737	probable CAAX pren
605	71	5.1	396	1	E64143	chloramphenicol re	678	70.5	5.1	480	2	S39978	scrA protein - Sta
606	71	5.1	397	2	C95221	hypothetical prote	679	70.5	5.1	491	2	AC1499	transmembrane prot
607	71	5.1	397	2	T00098	hypothetical prote	680	70.5	5.1	507	2	AB1707	glycine betaine tr
608	71	5.1	397	2	B98085	hypothetical prote	681	70.5	5.1	507	2	B64433	probable O-antigen
609	71	5.1	448	2	T30982	hypothetical prote	682	70.5	5.1	508	2	D81325	probable phosphate
610	71	5.1	458	2	AF0631	probable 4-hydroxy	683	70.5	5.1	533	2	S51171	amino acid transpo
611	71	5.1	461	2	S60253	sel-12 protein - C	684	70.5	5.1	585	2	C82955	probable sodium/pr
612	71	5.1	466	2	E90046	hypothetical prote	685	70.5	5.1	593	2	JT0974	cytochrome-c oxida
613	71	5.1	468	2	I64182	Na+/H+-exchanging	686	70.5	5.1	593	2	F84223	cytochrome-c oxida

687	70.5	5.1	674	2	AC1913	two-component sens	760	70	5.0	2201	1	GNNYA9	genome polyprotein
688	70.5	5.1	683	2	T12158	NADH2 dehydrogenas	761	69.5	5.0	202	2	F86347	hypothetical prote
689	70.5	5.1	704	2	T13581	NADH2 dehydrogenas	762	69.5	5.0	210	2	H81406	probable integral
690	70.5	5.1	718	2	S48726	phenylalanine ammo	763	69.5	5.0	215	2	S75345	hypothetical prote
691	70.5	5.1	733	2	T12213	NADH2 dehydrogenas	764	69.5	5.0	222	2	E72228	hypothetical prote
692	70.5	5.1	737	2	T13504	NADH2 dehydrogenas	765	69.5	5.0	224	2	B71191	hypothetical prote
693	70.5	5.1	738	2	C95936	conserved hypothet	766	69.5	5.0	256	2	S26742	tonoplast intrinsi
694	70.5	5.1	740	1	DENTN5	NADH2 dehydrogenas	767	69.5	5.0	260	2	G64690	type IIS restricti
695	70.5	5.1	741	2	T12610	NADH2 dehydrogenas	768	69.5	5.0	265	2	AF2007	hypothetical prote
696	70.5	5.1	741	2	T12702	NADH2 dehydrogenas	769	69.5	5.0	268	2	A70417	hypothetical prote
697	70.5	5.1	741	2	T13233	NADH2 dehydrogenas	770	69.5	5.0	285	1	C32804	prephenate dehydra
698	70.5	5.1	741	2	T13569	NADH2 dehydrogenas	771	69.5	5.0	285	2	AE1488	Staphylococcus xyl
699	70.5	5.1	921	2	T19694	hypothetical prote	772	69.5	5.0	286	2	F87075	membrane transport
700	70.5	5.1	1134	2	A41350	adenylate cyclase	773	69.5	5.0	287	2	T09791	drought-induced ma
701	70.5	5.1	1681	2	A55138	sodium channel mNa	774	69.5	5.0	292	2	G75288	hypothetical prote
702	70.5	5.1	1781	1	A34374	DNA-directed RNA p	775	69.5	5.0	294	2	S76277	ycf38 protein - Sy
703	70.5	5.1	2143	2	G96595	hypothetical prote	776	69.5	5.0	308	2	S16648	dipeptide transpor
704	70	5.0	98	2	T17099	NADH2 dehydrogenas	777	69.5	5.0	315	2	F72374	conserved hypothet
705	70	5.0	160	2	F72322	hypothetical prote	778	69.5	5.0	317	2	S72851	hypothetical prote
706	70	5.0	169	2	AB2739	acetyltransferase	779	69.5	5.0	325	2	T14227	NADH2 dehydrogenas
707	70	5.0	209	2	H97519	hypothetical prote	780	69.5	5.0	329	2	T11350	NADH2 dehydrogenas
708	70	5.0	240	1	QOBEG3	HWLF4 protein - hu	781	69.5	5.0	334	2	T19955	hypothetical prote
709	70	5.0	245	2	A90527	hypothetical prote	782	69.5	5.0	340	2	AE0353	probable membrane
710	70	5.0	250	2	C91020	hypothetical prote	783	69.5	5.0	351	2	T11794	NADH2 dehydrogenas
711	70	5.0	251	2	AH0575	2,3-dihydro-2,3-di	784	69.5	5.0	353	2	S65297	probable membrane
712	70	5.0	254	2	B70235	hypothetical prote	785	69.5	5.0	358	2	T29744	hypothetical prote
713	70	5.0	273	2	A72378	conserved hypothet	786	69.5	5.0	371	2	H97452	cytochrome c oxida
714	70	5.0	282	2	A99205	hypothetical prote	787	69.5	5.0	372	2	G82790	hypothetical prote
715	70	5.0	287	2	T12440	mipC protein - com	788	69.5	5.0	385	2	AE2717	permease [imported
716	70	5.0	320	2	T20176	hypothetical prote	789	69.5	5.0	385	2	H97498	permease AGR_C_211
717	70	5.0	325	2	C98135	hypothetical prote	790	69.5	5.0	393	1	A48357	nonstructural prot
718	70	5.0	325	2	AH3152	hypothetical prote	791	69.5	5.0	398	2	C90349	multidrug-efflux t
719	70	5.0	344	2	AE3228	agrocinopine synth	792	69.5	5.0	415	2	A39412	tryptophan transpo
720	70	5.0	344	2	S51948	hypothetical prote	793	69.5	5.0	420	2	AI2458	hypothetical prote
721	70	5.0	345	2	H95381	probable iron upta	794	69.5	5.0	426	2	E86575	phosphate permease
722	70	5.0	397	2	AF2016	hypothetical prote	795	69.5	5.0	439	2	A64769	branched-chain ami
723	70	5.0	413	2	H81659	branched-chain ami	796	69.5	5.0	439	2	C90685	branched-chain ami
724	70	5.0	427	2	S74444	hypothetical prote	797	69.5	5.0	439	2	G85535	branched-chain ami
725	70	5.0	442	2	E85864	probable transport	798	69.5	5.0	440	2	H90253	NADH-Ubiquinone/pl
726	70	5.0	443	2	H85485	probable transport	799	69.5	5.0	443	2	AG1335	hypothetical prote
727	70	5.0	443	2	H90634	probable transport	800	69.5	5.0	448	2	A69747	ABC transporter (p
728	70	5.0	456	2	F97810	magnesium transpor	801	69.5	5.0	458	2	B81409	probable transmemb
729	70	5.0	458	2	A37869	alpha-2B-adrenergi	802	69.5	5.0	459	2	S10196	NADH2 dehydrogenas
730	70	5.0	459	2	T11110	NADH2 dehydrogenas	803	69.5	5.0	470	2	C87683	conserved hypothet
731	70	5.0	459	2	S28025	light harvesting c	804	69.5	5.0	472	2	B91091	L-arabinose isomer
732	70	5.0	467	2	F91228	probable permease	805	69.5	5.0	472	2	E85936	L-arabinose isomer
733	70	5.0	503	2	AB2734	NADH dehydrogenase	806	69.5	5.0	472	2	B26430	L-arabinose isomer
734	70	5.0	503	2	D97515	NADH dehydrogenase	807	69.5	5.0	475	2	E83450	cytochrome-c oxida
735	70	5.0	519	2	F84222	quinone oxidoreduc	808	69.5	5.0	475	2	D83128	cytochrome-c oxida
736	70	5.0	522	2	B83987	ABC transporter (p	809	69.5	5.0	478	2	AC3395	NADH2 dehydrogenas
737	70	5.0	539	2	E97025	spoVB related memb	810	69.5	5.0	482	2	T45295	cytochrome-c oxida
738	70	5.0	539	2	S67049	probable membrane	811	69.5	5.0	493	2	S52421	amino acid transpo
739	70	5.0	576	2	B71420	hypothetical prote	812	69.5	5.0	507	2	T48645	glycine betaine tr
740	70	5.0	600	2	T32343	hypothetical prote	813	69.5	5.0	507	2	AD1336	glycine betaine tr
741	70	5.0	614	2	B84949	NADH2 dehydrogenas	814	69.5	5.0	515	2	T03717	GTP-binding protei
742	70	5.0	658	2	B86599	metal transport P-	815	69.5	5.0	536	2	A71491	probable integral
743	70	5.0	658	2	D72026	metal transport p-	816	69.5	5.0	570	2	S42708	proline transport
744	70	5.0	670	2	JQ1447	NADH2 dehydrogenas	817	69.5	5.0	570	2	S04547	proline transport
745	70	5.0	683	2	C81515	cation-transportin	818	69.5	5.0	572	2	AB2671	cytochrome-c oxida
746	70	5.0	688	2	T12670	NADH2 dehydrogenas	819	69.5	5.0	591	2	S14115	NADH2 dehydrogenas
747	70	5.0	698	2	T12556	NADH2 dehydrogenas	820	69.5	5.0	591	2	S43506	hypothetical prote
748	70	5.0	700	2	T13702	NADH2 dehydrogenas	821	69.5	5.0	615	2	S77332	NADH2 dehydrogenas
749	70	5.0	705	2	T13494	NADH2 dehydrogenas	822	69.5	5.0	627	2	T11125	NADH2 dehydrogenas
750	70	5.0	732	2	T12194	NADH2 dehydrogenas	823	69.5	5.0	627	2	S67257	proline transport
751	70	5.0	738	2	T14230	NADH2 dehydrogenas	824	69.5	5.0	631	2	S75742	hypothetical prote
752	70	5.0	744	2	A81719	exodeoxyribonuclea	825	69.5	5.0	643	2	S70592	NADH2 dehydrogenas
753	70	5.0	782	2	T25925	hypothetical prote	826	69.5	5.0	654	2	T14202	NADH2 dehydrogenas
754	70	5.0	836	2	E89453	protein F35H12.3 [	827	69.5	5.0	686	2	T13680	NADH2 dehydrogenas
755	70	5.0	860	2	AB2044	adenylate cyclase	828	69.5	5.0	701	2	T12296	NADH2 dehydrogenas
756	70	5.0	1018	2	T19693	hypothetical prote	829	69.5	5.0	718	2	A99195	hypothetical prote
757	70	5.0	1070	2	B86922	probable arabinosy	830	69.5	5.0	736	2	T12214	NADH2 dehydrogenas
758	70	5.0	1155	2	B71720	hypothetical prote	831	69.5	5.0	741	2	T12706	NADH2 dehydrogenas
759	70	5.0	2108	2	S72458	sodium channel pro	832	69.5	5.0	741	2	T13086	NADH2 dehydrogenas



833	69.5	5.0	741	2	T13372	NADH2 dehydrogenas	906	69	5.0	670	1	DN0B5	NADH2 dehydrogenas
834	69.5	5.0	744	2	T13682	NADH2 dehydrogenas	907	69	5.0	677	2	T11231	NADH2 dehydrogenas
835	69.5	5.0	747	2	E91049	probable cytochrom	908	69	5.0	684	2	T13695	NADH2 dehydrogenas
836	69.5	5.0	747	2	A85894	probable cytochrom	909	69	5.0	691	2	T12293	NADH2 dehydrogenas
837	69.5	5.0	809	1	SYBYQT	glutamine-tRNA lig	910	69	5.0	692	2	H71494	probable thiol-dis
838	69.5	5.0	970	2	A13605	potassium efflux s	911	69	5.0	702	2	T13505	NADH2 dehydrogenas
839	69.5	5.0	1302	2	B41249	multidrug resistanc	912	69	5.0	724	2	B83342	hypothetical prote
840	69.5	5.0	1645	2	T31339	carbamoyl-phosphat	913	69	5.0	737	2	T12193	NADH2 dehydrogenas
841	69.5	5.0	1827	2	A35694	cut1 protein - fis	914	69	5.0	777	2	AF2410	serine/threonine k
842	69.5	5.0	1828	2	T41455	cut1 protein - fis	915	69	5.0	903	2	AI0015	maltose regulon po
843	69	5.0	139	2	T31033	hypothetical prote	916	69	5.0	904	2	A84212	hypothetical prote
844	69	5.0	171	2	AF2434	hypothetical prote	917	69	5.0	975	2	T22788	hypothetical prote
845	69	5.0	233	2	S77443	cytochrome-c oxida	918	68.5	4.9	179	2	AD2573	hypothetical prote
846	69	5.0	233	2	AH1068	probable membrane	919	68.5	4.9	212	2	AE1473	hypothetical prote
847	69	5.0	236	2	S42069	TSGT protein - rat	920	68.5	4.9	278	2	T11550	probable membrane
848	69	5.0	254	2	C84315	hypothetical prote	921	68.5	4.9	289	2	D87933	protein R06C1.2 li
849	69	5.0	260	2	AG0434	probable membrane	922	68.5	4.9	295	2	T01528	probable plasma me
850	69	5.0	281	2	D64426	phosphate transpor	923	68.5	4.9	296	2	E69025	conserved hypothet
851	69	5.0	288	2	H72092	prolipoprotein dia	924	68.5	4.9	303	2	AG1396	cation transport p
852	69	5.0	288	2	G86529	prolipoprotein dia	925	68.5	4.9	305	2	S66005	conserved hypothet
853	69	5.0	290	2	T09260	aquaporin-like tra	926	68.5	4.9	313	2	C71545	probable oligopept
854	69	5.0	292	2	D81575	prolipoprotein dia	927	68.5	4.9	333	2	S52960	NADH2 dehydrogenas
855	69	5.0	296	1	BVECPT	prolipoprotein dia	928	68.5	4.9	336	2	I64096	transmembrane pore
856	69	5.0	296	2	F91211	phosphate transpor	929	68.5	4.9	346	2	B98135	hypothetical prote
857	69	5.0	296	2	F86057	hypothetical prote	930	68.5	4.9	346	2	AI3152	hypothetical prote
858	69	5.0	299	2	T06960	probable membrane	931	68.5	4.9	347	2	G96741	unknown protein F1
859	69	5.0	305	2	F70030	conserved hypothet	932	68.5	4.9	352	2	T23962	hypothetical prote
860	69	5.0	308	2	C86561	phosphatidate cyti	933	68.5	4.9	365	2	C97088	spore germination
861	69	5.0	308	2	H72062	phosphatidate cyti	934	68.5	4.9	367	2	T14228	NADH2 dehydrogenas
862	69	5.0	313	2	H71341	conserved hypothet	935	68.5	4.9	372	2	AB0276	probable membrane
863	69	5.0	347	2	T29415	hypothetical prote	936	68.5	4.9	383	2	C83436	probable MFS metab
864	69	5.0	364	2	D96973	spore germination	937	68.5	4.9	401	2	G95968	probable transport
865	69	5.0	369	2	F69478	NADH2 dehydrogenas	938	68.5	4.9	407	2	A69188	ammonium transport
866	69	5.0	387	2	E83679	multidrug-efflux t	939	68.5	4.9	454	2	AE1244	acetyl-CoA carboxy
867	69	5.0	389	2	T51355	membrane protein l	940	68.5	4.9	454	2	AI1606	acetyl-CoA carboxy
868	69	5.0	391	2	AB1285	transmembrane tran	941	68.5	4.9	455	2	F97065	D-xylose-proton sy
869	69	5.0	396	2	F83130	probable MFS trans	942	68.5	4.9	459	2	B95009	potassium uptake p
870	69	5.0	397	2	E81223	conserved hypothet	943	68.5	4.9	459	2	F97880	hypothetical prote
871	69	5.0	411	2	F97088	probable transmemb	944	68.5	4.9	462	2	H81952	probable integral
872	69	5.0	416	2	C81324	sugar-proton sympo	945	68.5	4.9	468	2	AF2163	hypothetical prote
873	69	5.0	429	2	AI0792	ubiquinol-cytochro	946	68.5	4.9	475	2	C83452	cytochrome-c oxida
874	69	5.0	431	2	A84380	probable transport	947	68.5	4.9	487	2	E97747	NADH2 dehydrogenas
875	69	5.0	432	2	C85087	hypothetical prote	948	68.5	4.9	488	1	QXASB1	mRNA maturase bil
876	69	5.0	443	2	E64725	hypothetical prote	950	68.5	4.9	489	2	E89102	protein F25E5.11 l
877	69	5.0	449	2	AB1707	yaaU protein - Bsc	951	68.5	4.9	507	2	B69316	DNA gyrase, subuni
878	69	5.0	451	2	E81781	FPS system galacti	952	68.5	4.9	509	2	T41034	probable WD-domain
879	69	5.0	451	2	A81206	probable integral	953	68.5	4.9	537	2	AI1277	probable transport
880	69	5.0	451	2	B90619	sugar transporter,	954	68.5	4.9	546	2	G86440	hypothetical prote
881	69	5.0	455	2	B96643	NADH dehydrogenase	955	68.5	4.9	597	2	T41501	major facilitator
882	69	5.0	458	2	D86814	hypothetical prote	956	68.5	4.9	616	2	F90371	amino acid transpo
883	69	5.0	462	2	D86814	transport protein	957	68.5	4.9	627	2	C96981	ABC transporter AT
884	69	5.0	464	2	C40630	GDP-mannose pyroph	958	68.5	4.9	637	2	AC3217	potassium uptake p
885	69	5.0	473	2	T03611	cyclin, B-type - c	959	68.5	4.9	685	2	T12129	NADH2 dehydrogenas
886	69	5.0	478	2	T29174	hypothetical prote	960	68.5	4.9	687	2	T12126	NADH2 dehydrogenas
887	69	5.0	482	2	C90067	hypothetical prote	961	68.5	4.9	688	2	T13242	NADH2 dehydrogenas
888	69	5.0	483	2	A81352	integral membrane	962	68.5	4.9	688	2	T13373	NADH2 dehydrogenas
889	69	5.0	487	2	S40820	probable permease	963	68.5	4.9	689	2	T13681	NADH2 dehydrogenas
890	69	5.0	488	1	H64537	cytochrome-c oxida	964	68.5	4.9	698	2	T13492	NADH2 dehydrogenas
891	69	5.0	488	2	G71969	cytochrome-c oxida	965	68.5	4.9	701	2	F70155	Na+/H+ antiporter
892	69	5.0	492	2	AD3055	succinoglycan bios	966	68.5	4.9	716	2	E82016	probable integral
893	69	5.0	495	2	S75340	NADH2 dehydrogenas	967	68.5	4.9	721	2	B83820	hypothetical prote
894	69	5.0	498	2	H82494	probable NADH dehy	968	68.5	4.9	736	2	T12225	NADH2 dehydrogenas
895	69	5.0	509	2	D86978	hypothetical prote	969	68.5	4.9	736	2	T12222	NADH2 dehydrogenas
896	69	5.0	516	2	G82182	probable NADH dehy	970	68.5	4.9	741	2	T12711	NADH2 dehydrogenas
897	69	5.0	522	2	A98231	succinoglycan bios	971	68.5	4.9	741	2	T12620	NADH2 dehydrogenas
898	69	5.0	528	2	T34941	probable Na+/H+ an	972	68.5	4.9	741	2	T12699	NADH2 dehydrogenas
899	69	5.0	554	2	S03809	cytochrome-c oxida	973	68.5	4.9	743	2	T13700	NADH2 dehydrogenas
900	69	5.0	588	2	A43740	DG42 protein - Afr	974	68.5	4.9	743	2	T12760	NADH2 dehydrogenas
901	69	5.0	591	2	G97748	virD4 protein [imp	975	68.5	4.9	744	2	T12705	NADH2 dehydrogenas
902	69	5.0	605	2	H95240	conserved hypothet	976	68.5	4.9	745	2	G84995	vacB protein [impo
903	69	5.0	605	2	A99705	hypothetical prote	977	68.5	4.9	746	2	C95110	competence protein
904	69	5.0	642	2	T33262	hypothetical prote	978	68.5	4.9	747	2	T13683	NADH2 dehydrogenas
905	69	5.0	652	2	C97087	probable permease	978	68.5	4.9	750	2	B90137	sulfate permease l

979	68.5	4.9	820	2	D71471	probable DNA misma	1052	68	4.9	899	2	S76449	hypothetical prote
980	68.5	4.9	827	2	A95877	hypothetical prote	1053	68	4.9	906	2	S35342	Golgi-associated p
981	68.5	4.9	870	2	A89201	protein F32D8.4 [i	1054	68	4.9	999	2	F72453	probable cytochrom
982	68.5	4.9	874	2	JQ0883	genome polyprotein	1055	68	4.9	1039	2	C87083	C-term lysyl-tRNA
983	68.5	4.9	881	2	AE2777	potassium efflux s	1056	68	4.9	1082	2	T45096	probable arabinosy
984	68.5	4.9	881	2	B97557	hypothetical prote	1057	68	4.9	1323	2	T18214	ATP binding casses
985	68.5	4.9	912	2	T21659	hypothetical prote	1058	68	4.9	1368	2	T51622	probable aldehyde
986	68.5	4.9	960	2	A82142	probable cell divi	1059	68	4.9	1541	1	S71839	canalicular multib
987	68.5	4.9	1081	2	T52028	cellulose synthase	1060	67.5	4.8	100	2	B69836	hypothetical prote
988	68.5	4.9	1084	2	T08583	cellulose synthase	1061	67.5	4.8	212	2	AI1111	hypothetical prote
989	68.5	4.9	1394	2	S66876	ATP-dependent tran	1062	67.5	4.8	269	2	E72693	hypothetical prote
990	68.5	4.9	1504	2	A33602	DNA-directed DNA p	1063	67.5	4.8	284	2	AC1198	Streptococcus agal
991	68	4.9	148	2	S74589	hypothetical prote	1064	67.5	4.8	288	2	T33224	hypothetical prote
992	68	4.9	183	2	T49855	hypothetical prote	1065	67.5	4.8	291	2	B95316	probable ABC trans
993	68	4.9	214	2	G83882	hypothetical prote	1066	67.5	4.8	293	2	D81673	ABC transporter, p
994	68	4.9	215	2	S16564	nolH protein - Rhi	1067	67.5	4.8	300	2	G70943	hypothetical prote
995	68	4.9	237	2	H86841	transport permease	1068	67.5	4.8	302	2	G90078	hypothetical prote
996	68	4.9	241	2	T33804	hypothetical prote	1069	67.5	4.8	302	2	G71660	hypothetical prote
997	68	4.9	252	2	A70529	hypothetical prote	1070	67.5	4.8	302	2	AF2686	ABC transporter, m
998	68	4.9	254	2	E70438	type 4 prepilin pe	1071	67.5	4.8	302	2	C97468	probable permease
999	68	4.9	256	2	C72261	spermidine/putresc	1072	67.5	4.8	304	2	AD1029	probable membrane
1000	68	4.9	265	2	AD0214	PTS system, mannos	1073	67.5	4.8	307	2	C70952	probable sugA prot
1001	68	4.9	265	2	E82716	ATP synthase, A ch	1074	67.5	4.8	310	2	A86812	sugar ABC transpor
1002	68	4.9	282	2	AD0848	iron transport pro	1075	67.5	4.8	314	2	AB2230	hypothetical prote
1003	68	4.9	286	2	D83914	chloramphenicol re	1076	67.5	4.8	323	2	T31828	hypothetical prote
1004	68	4.9	296	2	AD0956	phosphate transpor	1077	67.5	4.8	327	1	S45529	NADPH2:quinone red
1005	68	4.9	304	2	A89905	hypothetical prote	1078	67.5	4.8	327	2	S67168	probable membrane
1006	68	4.9	312	2	F70044	hypothetical prote	1079	67.5	4.8	344	2	T32600	hypothetical prote
1007	68	4.9	316	2	S50336	NADH2 dehydrogenas	1080	67.5	4.8	347	2	T28733	hypothetical prote
1008	68	4.9	316	2	E81321	probable cation tr	1081	67.5	4.8	349	2	S51267	probable galactosy
1009	68	4.9	329	2	F98334	SN-glycerol 3-phos	1082	67.5	4.8	359	2	I51372	angiotensin II rec
1010	68	4.9	335	2	S44635	f22b7.7 protein -	1083	67.5	4.8	361	2	D72384	conserved hypothet
1011	68	4.9	353	2	T06515	probable adenosylm	1084	67.5	4.8	364	1	S77360	cblD protein - Syn
1012	68	4.9	357	2	C97744	hypothetical prote	1085	67.5	4.8	367	2	T23290	hypothetical prote
1013	68	4.9	358	2	T38914	para-hydroxybenzoa	1086	67.5	4.8	374	2	G86044	EspD protein limpo
1014	68	4.9	396	2	AF0677	probable membrane	1087	67.5	4.8	374	2	C91198	secreted protein E
1015	68	4.9	396	2	A91019	probable antibioti	1088	67.5	4.8	377	2	T21170	hypothetical prote
1016	68	4.9	396	2	C85863	probable antibioti	1089	67.5	4.8	379	2	D81515	cell shape-determi
1017	68	4.9	397	2	G90013	hypothetical prote	1090	67.5	4.8	387	2	JE0364	lactosylceramide a
1018	68	4.9	408	2	AC1373	conserved hypothet	1091	67.5	4.8	393	2	T12608	NADH2 dehydrogenas
1019	68	4.9	417	2	E82966	tryptophan permeas	1092	67.5	4.8	402	2	B69843	conserved hypothet
1020	68	4.9	437	1	F64614	conserved hypothet	1093	67.5	4.8	409	2	AF3271	probable allantoin
1021	68	4.9	442	2	H81402	probable integral	1094	67.5	4.8	415	2	F91209	low affinity trypt
1022	68	4.9	448	2	G70172	conserved hypothet	1095	67.5	4.8	415	2	A86056	low affinity trypt
1023	68	4.9	461	2	H82186	probable multidrug	1096	67.5	4.8	415	2	A86599	rod shape protein
1024	68	4.9	469	2	C69628	gamma-aminobutyrat	1097	67.5	4.8	415	2	C72026	rod shape protein
1025	68	4.9	476	2	D83600	probable aldehyde	1098	67.5	4.8	415	2	H71841	hypothetical prote
1026	68	4.9	485	2	T24115	hypothetical prote	1099	67.5	4.8	426	2	A96000	probable C4-dicarb
1027	68	4.9	488	1	QXASM4	NADH2 dehydrogenas	1100	67.5	4.8	456	2	E83750	gluconate permease
1028	68	4.9	489	2	B53153	glucose transport	1101	67.5	4.8	456	2	B83391	probable amino aci
1029	68	4.9	494	2	JC2382	sodium/proline sym	1102	67.5	4.8	459	2	S47879	NADH2 dehydrogenas
1030	68	4.9	505	2	B97747	NADH2 dehydrogenas	1103	67.5	4.8	462	2	D81010	conserved hypothet
1031	68	4.9	512	2	G90399	amino acid transpo	1104	67.5	4.8	463	2	A69905	conserved hypothet
1032	68	4.9	521	2	E64181	probable cytochrom	1105	67.5	4.8	463	2	E83242	probable adenylate
1033	68	4.9	523	2	T12198	sucrose transport	1106	67.5	4.8	467	2	AB2493	hypothetical prote
1034	68	4.9	534	2	S64593	probable membrane	1107	67.5	4.8	467	2	A81263	probable integral
1035	68	4.9	537	2	AH1640	probable transport	1108	67.5	4.8	477	2	D83617	probable amino aci
1036	68	4.9	550	2	T37519	probable amino aci	1109	67.5	4.8	483	2	AI0449	protein-Npi-phosph
1037	68	4.9	564	2	C83742	cytochrome c oxida	1110	67.5	4.8	486	2	F71683	NADH2 dehydrogenas
1038	68	4.9	592	2	E70488	cytochrome-c oxida	1111	67.5	4.8	490	2	E82740	C4-dicarboxylate t
1039	68	4.9	593	2	S26696	alkaline proteinas	1112	67.5	4.8	495	2	B81297	sodium/proline sym
1040	68	4.9	600	2	C69371	conserved hypothet	1113	67.5	4.8	501	2	T02134	hypothetical prote
1041	68	4.9	602	2	T13679	NADH2 dehydrogenas	1114	67.5	4.8	510	2	H87320	conserved hypothet
1042	68	4.9	617	2	F82744	ferrous iron trans	1115	67.5	4.8	512	2	S28663	cytochrome-c oxida
1043	68	4.9	633	2	I58140	glycine transporte	1116	67.5	4.8	513	2	I45456	NADH2 dehydrogenas
1044	68	4.9	633	2	S45877	uracil transport p	1117	67.5	4.8	514	2	T46131	4-coumarate-CoA li
1045	68	4.9	638	2	JH0673	glycine transport	1118	67.5	4.8	519	1	S02153	NADH2 dehydrogenas
1046	68	4.9	683	2	T12295	NADH2 dehydrogenas	1119	67.5	4.8	552	2	E70731	probable pitB prot
1047	68	4.9	688	2	T13278	NADH2 dehydrogenas	1120	67.5	4.8	560	2	F81423	L-lactate permease
1048	68	4.9	689	2	T13762	NADH2 dehydrogenas	1121	67.5	4.8	568	2	JC7911	Na+-coupled citrat
1049	68	4.9	705	2	T12152	NADH2 dehydrogenas	1122	67.5	4.8	615	2	H82635	hypothetical prote
1050	68	4.9	709	2	A97218	uncharacterized co	1123	67.5	4.8	617	2	B82285	protein-export mem
1051	68	4.9	811	2	T36581	probable transmemb	1124	67.5	4.8	631	2	H70754	probable abc trans

1125	67.5	4.8	637	2	JH0674	L-proline transpor	1198	67	4.8	406	2	H89006	protein T22F3.11 [
1126	67.5	4.8	645	2	T12159	NADH2 dehydrogenas	1199	67	4.8	407	2	AD0706	O-antigen polymera
1127	67.5	4.8	645	2	A75390	NADH2 dehydrogenas	1200	67	4.8	407	2	A43672	O-antigen polymera
1128	67.5	4.8	659	2	T33557	hypothetical prote	1201	67	4.8	409	2	C82644	transcription regu
1129	67.5	4.8	690	2	D75487	v-type ATP synthas	1202	67	4.8	411	2	S61245	probable virion gl
1130	67.5	4.8	699	2	T12169	NADH2 dehydrogenas	1203	67	4.8	416	2	JN0720	glucosyl transfera
1131	67.5	4.8	703	2	T13074	NADH2 dehydrogenas	1204	67	4.8	417	2	H83708	hypothetical prote
1132	67.5	4.8	741	2	T13404	NADH2 dehydrogenas	1205	67	4.8	421	2	AF2382	hypothetical prote
1133	67.5	4.8	741	2	T13760	NADH2 dehydrogenas	1206	67	4.8	423	2	E82611	conserved hypothet
1134	67.5	4.8	741	2	T13776	NADH2 dehydrogenas	1207	67	4.8	430	2	S74039	hypothetical prote
1135	67.5	4.8	741	2	T12762	NADH2 dehydrogenas	1208	67	4.8	446	2	AC3349	protein translocas
1136	67.5	4.8	744	2	T12694	NADH2 dehydrogenas	1209	67	4.8	453	2	A43765	stsl+ protein - fi
1137	67.5	4.8	744	2	T12611	NADH2 dehydrogenas	1210	67	4.8	453	2	T30985	hypothetical prote
1138	67.5	4.8	801	2	A89862	Na+/H+ antiporter	1211	67	4.8	456	2	AI2789	manganese transpor
1139	67.5	4.8	812	2	T19446	hypothetical prote	1212	67	4.8	458	2	H71657	NADH2 dehydrogenas
1140	67.5	4.8	820	2	G82168	trimethylamine-N-o	1213	67	4.8	459	1	DNHUN4	NADH2 dehydrogenas
1141	67.5	4.8	823	2	S44873	ZC21.2 protein - C	1214	67	4.8	461	2	H97568	manganese transpor
1142	67.5	4.8	823	2	B81282	probable integral	1215	67	4.8	462	2	T34365	hypothetical prote
1143	67.5	4.8	890	2	H69877	calcium-transporti	1216	67	4.8	468	2	AD0521	probable symporter
1144	67.5	4.8	900	2	D97351	sensor protein Kdp	1217	67	4.8	469	2	T35670	hypothetical prote
1145	67.5	4.8	936	2	B64567	cytochrome c bioge	1218	67	4.8	470	2	T26602	hypothetical prote
1146	67.5	4.8	952	2	T32836	hypothetical prote	1219	67	4.8	473	2	AG0612	probable transpor
1147	67.5	4.8	1199	1	S76549	transcription-repa	1220	67	4.8	477	2	S71323	alpha-1A adrenergi
1148	67.5	4.8	1247	1	VHWV2	structural polypro	1221	67	4.8	485	2	C70488	cytochrome-c oxida
1149	67.5	4.8	1517	1	F65112	glutamate synthase	1222	67	4.8	491	2	G69251	proline permease (
1150	67.5	4.8	1517	2	F85985	glutamate synthase	1223	67	4.8	494	2	AC0133	probable permease
1151	67.5	4.8	1517	2	C91140	glutamate synthase	1224	67	4.8	511	2	H90439	hypothetical prote
1152	67.5	4.8	1704	2	T42749	ATP-binding casset	1225	67	4.8	516	2	T33269	hypothetical prote
1153	67.5	4.8	1767	2	S60124	transport protein	1226	67	4.8	517	2	AC2070	Na+/H+ antiporter
1154	67.5	4.8	1778	2	AF1116	internalin protein	1227	67	4.8	517	2	E82147	hypothetical prote
1155	67.5	4.8	2701	2	S17796	inositol-trisphosp	1228	67	4.8	522	2	F86215	protein T6D22.18 [
1156	67	4.8	90	2	E82861	conjugal transfer	1229	67	4.8	527	2	T49241	pectinesterase-lik
1157	67	4.8	109	2	C98018	crcB protein limpo	1230	67	4.8	537	2	D70478	conserved hypothet
1158	67	4.8	168	2	A72226	conserved hypothet	1231	67	4.8	546	2	AE0571	probable membrane
1159	67	4.8	180	2	C86290	hypothetical prote	1232	67	4.8	557	2	T46520	probable transmemb
1160	67	4.8	187	2	A95143	membrane protein [	1233	67	4.8	557	2	S58688	probable transport
1161	67	4.8	187	2	G98010	conserved hypothet	1234	67	4.8	557	2	G69096	hypothetical prote
1162	67	4.8	226	2	S57521	probable arsenical	1235	67	4.8	574	2	T41068	hypothetical prote
1163	67	4.8	232	1	G64591	conserved hypothet	1236	67	4.8	574	2	T34208	hypothetical prote
1164	67	4.8	259	2	S59152	cytochrome-c oxida	1237	67	4.8	584	2	B82810	ABC transporter ni
1165	67	4.8	260	2	A91138	hypothetical prote	1238	67	4.8	605	2	A36361	glucose transport
1166	67	4.8	260	2	D65110	hypothetical 27.9	1239	67	4.8	625	2	T33792	hypothetical prote
1167	67	4.8	260	2	D85983	hypothetical prote	1240	67	4.8	625	2	AD2251	two-component sens
1168	67	4.8	261	2	T11826	cytochrome-c oxida	1241	67	4.8	640	2	D90174	hypothetical prote
1169	67	4.8	265	2	T05668	pollen allergen ho	1242	67	4.8	644	2	S44478	NADH2 dehydrogenas
1170	67	4.8	268	2	C86944	probable cation-ef	1243	67	4.8	653	2	T19245	hypothetical prote
1171	67	4.8	278	2	A99349	bacitracin resista	1244	67	4.8	659	2	C65022	yffg protein - Esc
1172	67	4.8	285	2	A84224	cytochrome c oxida	1245	67	4.8	698	2	T12586	NADH2 dehydrogenas
1173	67	4.8	287	2	B89936	hypothetical prote	1246	67	4.8	698	2	T12568	hypothetical prote
1174	67	4.8	288	2	I78556	membrane glycoprot	1247	67	4.8	698	2	S76532	NADH2 dehydrogenas
1175	67	4.8	291	2	S48977	hypothetical prote	1248	67	4.8	699	2	T13778	NADH2 dehydrogenas
1176	67	4.8	293	2	D86065	glucose-1-phosphat	1249	67	4.8	707	2	G86894	hypothetical prote
1177	67	4.8	293	2	B91219	glucose-1-phosphat	1250	67	4.8	741	1	S34218	1,4-alpha-glucan b
1178	67	4.8	293	2	H65182	glucose-1-phosphat	1251	67	4.8	741	2	T13764	NADH2 dehydrogenas
1179	67	4.8	308	2	H64409	hypothetical prote	1252	67	4.8	878	2	A87385	TonB-dependent rec
1180	67	4.8	313	2	T24994	hypothetical prote	1253	67	4.8	918	2	A44257	interleukin-6 sign
1181	67	4.8	313	2	C95247	conserved hypothet	1254	67	4.8	970	2	F64230	spore germination
1182	67	4.8	313	2	H98111	conserved hypothet	1255	67	4.8	1001	2	T13807	potassium channel
1183	67	4.8	314	2	F81699	peptide ABC transp	1256	67	4.8	1218	2	S38182	probable transport
1184	67	4.8	323	2	AB0427	octaprenyl-diphosp	1257	67	4.8	1440	2	JC6312	protein-tyrosine-p
1185	67	4.8	328	2	D72566	hypothetical prote	1258	67	4.8	1457	1	A48066	protein-tyrosine-p
1186	67	4.8	349	2	AD0990	probable membrane	1259	67	4.8	1489	2	S73015	polyketide synthas
1187	67	4.8	354	2	C82038	nitrogen regulatio	1260	67	4.8	1559	2	AI2348	ferredoxin-glutama
1188	67	4.8	356	2	B84749	hypothetical prote	1261	67	4.8	1758	2	F88559	protein C48B4.4b [
1189	67	4.8	364	2	T45253	probable antiporte	1262	67	4.8	2183	2	S47307	genome polyprotein
1190	67	4.8	364	2	T24418	hypothetical prote	1263	66.5	4.8	175	2	A95058	conserved domain p
1191	67	4.8	367	2	S23349	hypothetical prote	1264	66.5	4.8	175	2	B97927	hypothetical prote
1192	67	4.8	371	2	D97790	octaprenyl-diphosp	1265	66.5	4.8	185	2	D81327	probable integral
1193	67	4.8	377	2	B71699	cell division prot	1266	66.5	4.8	205	2	A87460	Deda family protei
1194	67	4.8	388	2	B64459	Na+/H+-exchanging	1267	66.5	4.8	217	2	B69396	hypothetical prote
1195	67	4.8	394	2	AH0020	conserved integral	1268	66.5	4.8	245	2	F71887	hypothetical prote
1196	67	4.8	397	2	B70763	probable membrane	1269	66.5	4.8	256	2	G82804	phosphatidyltransf
1197	67	4.8	401	2	H82175	multidrug resistan	1270	66.5	4.8	258	2	A69830	hypothetical prote

1271	66.5	4.8	261	2	I64249	hypothetical prote	1344	66.5	4.8	744	2	T13063	NADH2 dehydrogenas
1272	66.5	4.8	269	2	A86889	zinc ABC transport	1345	66.5	4.8	744	2	T13048	NADH2 dehydrogenas
1273	66.5	4.8	279	2	E69226	hypothetical prote	1346	66.5	4.8	746	2	T01536	hypothetical prote
1274	66.5	4.8	292	2	A70546	probable menA prot	1347	66.5	4.8	755	2	T20950	hypothetical prote
1275	66.5	4.8	292	2	F83823	hypothetical prote	1348	66.5	4.8	759	2	D70422	cellulose synthase
1276	66.5	4.8	293	2	T41928	hypothetical prote	1349	66.5	4.8	790	2	G90477	hypothetical prote
1277	66.5	4.8	295	2	AE0993	glycerol-3-phospha	1350	66.5	4.8	812	2	T16621	hypothetical prote
1278	66.5	4.8	306	2	C70141	oligopeptide ABC t	1351	66.5	4.8	820	2	T41978	helicase - human h
1279	66.5	4.8	306	2	S55047	ABC-type transport	1352	66.5	4.8	860	2	C82750	mannosyltransferas
1280	66.5	4.8	320	2	T23635	hypothetical prote	1353	66.5	4.8	919	2	SI9810	glutamate receptor
1281	66.5	4.8	361	2	T37938	hypothetical prote	1354	66.5	4.8	919	2	I53474	kainate receptor -
1282	66.5	4.8	366	2	G95376	conserved hypothet	1355	66.5	4.8	937	2	T37241	olfactory channel
1283	66.5	4.8	375	2	T05707	phosphate transpor	1356	66.5	4.8	957	2	D88651	protein B0212.5 [i
1284	66.5	4.8	385	2	B87441	rod shape-determin	1357	66.5	4.8	999	2	T27628	hypothetical prote
1285	66.5	4.8	389	2	AD1378	cell division prot	1358	66.5	4.8	1002	2	G97217	conserved membrane
1286	66.5	4.8	390	2	AH0260	conserved hypothet	1359	66.5	4.8	1010	1	PXZP2P	H+-exporting ATPas
1287	66.5	4.8	394	2	T13721	NADH2 dehydrogenas	1360	66.5	4.8	1049	2	T22762	hypothetical prote
1288	66.5	4.8	405	2	T40193	hypothetical prote	1361	66.5	4.8	1068	2	AB1082	B. subtilis YueB p
1289	66.5	4.8	409	2	B85735	probable membrane	1362	66.5	4.8	1088	2	H84604	probable cellulose
1290	66.5	4.8	410	2	E75290	probable multidrug	1363	66.5	4.8	1248	2	C89874	autolysin [impor
1291	66.5	4.8	411	2	S73218	preprotein translo	1364	66.5	4.8	1704	2	S71363	probable ATP-bindi
1292	66.5	4.8	421	2	E90883	hypothetical prote	1365	66.5	4.8	1704	2	A59188	ATP-binding casset
1293	66.5	4.8	422	2	H69839	multidrug resistan	1366	66	4.7	101	2	G69894	hypothetical prote
1294	66.5	4.8	428	2	G82918	hypothetical prote	1367	66	4.7	105	2	AH2209	hypothetical prote
1295	66.5	4.8	438	2	H91112	hypothetical prote	1368	66	4.7	158	2	S58016	probable olfactory
1296	66.5	4.8	438	2	H85957	partial probable t	1369	66	4.7	171	2	S44146	amiS protein - Pse
1297	66.5	4.8	440	2	C71863	probable aminotran	1370	66	4.7	172	2	A83226	hypothetical prote
1298	66.5	4.8	441	2	T19306	hypothetical prote	1371	66	4.7	195	1	CYHYAM	alpha-crystallin c
1299	66.5	4.8	452	2	D86835	maltose ABC transp	1372	66	4.7	196	2	AD2304	hypothetical prote
1300	66.5	4.8	454	2	A70079	conserved hypothet	1373	66	4.7	203	2	T05519	hypothetical prote
1301	66.5	4.8	467	2	F90544	conserved hypothet	1374	66	4.7	203	2	C85288	hypothetical prote
1302	66.5	4.8	467	2	T16319	hypothetical prote	1375	66	4.7	204	2	D69097	hypothetical prote
1303	66.5	4.8	469	2	H70626	probable narK3 pro	1376	66	4.7	211	2	E89963	hypothetical prote
1304	66.5	4.8	471	2	F71543	probable dicarboxy	1377	66	4.7	255	2	AH0577	molybdopterin-cont
1305	66.5	4.8	472	2	E83497	probable amino aci	1378	66	4.7	256	2	QJ1106	tonoplast intrinsi
1306	66.5	4.8	474	2	S07754	NADH2 dehydrogenas	1379	66	4.7	260	2	AG0904	probable membrane
1307	66.5	4.8	475	2	T46745	arginine/ornithine	1380	66	4.7	265	2	H90254	sulfate ABC transp
1308	66.5	4.8	478	2	D64895	probable membrane	1381	66	4.7	267	2	A87233	conserved membrane
1309	66.5	4.8	480	2	D90038	PTS system, sucros	1382	66	4.7	275	2	F83222	NosY protein PA339
1310	66.5	4.8	484	2	E75138	osmoregulated prol	1383	66	4.7	276	2	B35252	hema concentration
1311	66.5	4.8	491	2	H84379	4-hydroxybutyrate	1384	66	4.7	280	2	F75057	hypothetical prote
1312	66.5	4.8	492	2	T15603	hypothetical prote	1385	66	4.7	285	2	E84789	hypothetical prote
1313	66.5	4.8	498	2	AI0482	phosphate transpor	1386	66	4.7	285	2	D84789	hypothetical prote
1314	66.5	4.8	499	2	A65085	probable low-affin	1387	66	4.7	285	2	S44085	plasma membrane in
1315	66.5	4.8	509	2	T11043	cytochrome-c oxida	1388	66	4.7	296	2	G72760	hypothetical prote
1316	66.5	4.8	513	2	T14864	probable monosacch	1389	66	4.7	298	2	T13684	NADH2 dehydrogenas
1317	66.5	4.8	513	2	C81859	probable integral	1390	66	4.7	303	2	AB1772	cation transport p
1318	66.5	4.8	519	2	E90548	conserved hypothet	1391	66	4.7	307	2	T16457	hypothetical prote
1319	66.5	4.8	520	2	D90014	hypothetical prote	1392	66	4.7	311	2	AI2697	permease [impor
1320	66.5	4.8	526	2	H85891	hydrogenase 4 memb	1393	66	4.7	311	2	B97480	hypothetical prote
1321	66.5	4.8	526	2	E65024	Hydrogenase-4 comp	1394	66	4.7	312	2	G69423	branched-chain ami
1322	66.5	4.8	530	2	T11884	cytochrome-c oxida	1395	66	4.7	312	2	H90517	hypothetical prote
1323	66.5	4.8	553	2	T38541	probable sucrose c	1396	66	4.7	318	2	AI1811	hypothetical prote
1324	66.5	4.8	557	2	T49811	probable vacuolar	1397	66	4.7	320	2	T25308	hypothetical prote
1325	66.5	4.8	569	2	T37706	probable sodium/hy	1398	66	4.7	322	2	T13486	NADH2 dehydrogenas
1326	66.5	4.8	573	2	T23102	hypothetical prote	1399	66	4.7	330	1	H69798	conserved hypothet
1327	66.5	4.8	574	2	G84578	probable potassium	1400	66	4.7	335	2	T39425	hypothetical prote
1328	66.5	4.8	648	2	C97961	DNA topoisomerase	1401	66	4.7	336	2	T31762	hypothetical prote
1329	66.5	4.8	648	2	F95093	DNA gyrase chain B	1402	66	4.7	344	2	AB3236	hypothetical prote
1330	66.5	4.8	649	2	AB2154	hypothetical prote	1403	66	4.7	354	2	S70595	NADH2 dehydrogenas
1331	66.5	4.8	659	2	S67175	probable membrane	1404	66	4.7	355	2	A64138	rfe protein - Haem
1332	66.5	4.8	660	1	S54746	cytochrome c-type	1405	66	4.7	357	2	T03557	ribose transport s
1333	66.5	4.8	664	2	B53610	ntpi protein - Ent	1406	66	4.7	357	2	F81916	probable integral
1334	66.5	4.8	679	2	H95036	glycosyl hydrolase	1407	66	4.7	371	2	AD1201	N-acyl-L-amino aci
1335	66.5	4.8	699	2	T12173	NADH2 dehydrogenas	1408	66	4.7	377	2	H64387	hypothetical prote
1336	66.5	4.8	703	2	H86588	thio,disulfide int	1409	66	4.7	381	2	C71680	hypothetical prote
1337	66.5	4.8	703	2	H72034	thiol-disulfide in	1410	66	4.7	383	2	E87680	hypothetical prote
1338	66.5	4.8	714	2	G81503	thiol-disulfide in	1411	66	4.7	395	2	A86527	neutral amino acid
1339	66.5	4.8	725	2	S52990	phenylalanine ammo	1412	66	4.7	395	2	E72095	neutral amino acid
1340	66.5	4.8	732	2	AD0014	primosomal protein	1413	66	4.7	396	2	AH2859	MFS permease [impo
1341	66.5	4.8	737	2	D97907	alpha-xylosidase (	1414	66	4.7	396	2	F97636	probable transport
1342	66.5	4.8	741	2	T12605	NADH2 dehydrogenas	1415	66	4.7	398	2	H75043	mg2+ transport pro
1343	66.5	4.8	741	2	T13361	NADH2 dehydrogenas	1416	66	4.7	404	2	S65991	membrane protein y







Db 848 FAIIAAMVAMALIRNLPGLLEVLVLSRLNMRQASVAITILNYVIAVGAAMTVFGLGV 907

Qy 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137

Db 908 SWDKLQWLAALSGLGFLQEIIFGNFVSGLIILFERPVRIGDVTVTIGTYSKIRIR 967

Qy 138 VQTILSYQMPKIHGKQVFWIRLLLVWCGVSALSMLTSCSSVLHSG-NFGTDLEQKLHWN 196

Db 968 ATTITDFDRKEVIIPNKAF-VTERLINW-----SLSDTTTTLRVIRLGVAYGSDLEK----- 1017

Qy 197 PEDKGVVLMHMITAA-----EWSMSFSFFGF-----FLTYIRDFQKISLRVE 238

Db 1018 -----VKRVLLQAAMEHPKVMHDPEPAVFFTTFGASTLDHELRLYVRELRDRSHTVD 1069

RESULT 6

E72523

carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: E72523

R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: E72523

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-604 <KAW>

A:Cross-references: UNIPROT:Q9Y9X7; UNIPARC:UPI000005E231; DBJ:AP0000063; NID:G5105654;

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE2162

C:Superfamily: carbon starvation protein

Query Match 7.0%; Score 97; DB 2; Length 604;

Best Local Similarity 23.9%; Pred. No. 1.1;

Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;

Qy 4 FQOGLSFLPSAL--VIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLN 61

Db 183 YRMGLGMGPSTVITVVLVIAAFVSYNHGIVIGTFDPSLP-PGEGGWAYHRWVI--ILG 239

Qy 62 IAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAAH 121

Db 240 LYALLA-ASLPVWY---LQPRD----YLNAYILWTG---LGLAAIA---AILLGTQS 283

Qy 122 VSGAVLTFMGSLYMFVQTILSYQMPKIHGKQVFWIRLLLVWCGVSALSMLTSCSSVLH 181

Db 284 LKGPAYT-----SFQPNIIAQPTP-----FWPAIPLIIACG----SLSGFHSLSVA 325

Qy 182 SGNFGTDLEQKLH-----WN-PE--DKGYV-LHMITTA 210

Db 326 SGTTSKQLASELDALFVGYGAMLEGALSGLAVIIPISPAWNAPELIQGVINNMLDLA 385

Qy 211 A-----EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDT 249

Db 386 AVPRYAVGYGYTLAKTFEMFGVGFDGTGYSFFTLFASLMSMYVLTLDLT 434

RESULT 7

S43882

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion

C:Species: mitochondrion Lactuca sativa (garden lettuce)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S43882

R:Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.

Mol. Gen. Genet. 243, 97-105, 1994

A:Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrial

A:Reference number: S43882; MUID:94247363; PMID:8190077

A:Accession: S43882

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-495 <GEI>

A:Cross-references: UNIPROT:Q37544; UNIPARC:UPI000008E589

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 96; DB 2; Length 495;

Best Local Similarity 24.6%; Pred. No. 1.1;

Matches 55; Conservative 34; Mismatches 83; Indels 52; Gaps 12;

Qy 8 LSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYLSAIAIYYTSLTTLRQID--LKKIIAYSSVAHNMNLVTIGMFSLNIQGI 331

Qy 63 -----AAVLCIATIIYRYKQ-----VHALSPEENVIIKLNKAGLVL 98

Db 332 GGSILLMLSHGLVSSALFLCVGLYVRHKTRLVRYYGGLVSTMPNFSTIFFFTLANMSL 391

Qy 99 -GILSCIG--LSIVANFQKTTLFAAHVSGAVLTFMGSLYMFVQTILSYQMP----- 148

Db 392 PGTSSFIGEFILVGAFQFQNSLVATLAALGMILGAAYSLLWLY-NRVVSGNLKPDFLHKFS 450

Qy 149 KIHGKQVF-WIRLLL-VIWCVSALSMLTC-----SSVLHSGNF 185

Db 451 DLNGTEVFIFIPFLVGVVMGVYPKVPFDCMHTSVSNLVQHCKF 494

RESULT 8

S16447

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion

N:Alternate names: mitochondrial complex I subunit IV

C:Species: mitochondrion Triticum aestivum (common wheat)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: S16447; S16448; S06835

R:Lamattina, L.; Grienemberger, J.M.

Nucleic Acids Res. 19, 3275-3282, 1991

A:Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in whe

A:Reference number: S16447; MUID:91288205; PMID:1712098

A:Accession: S16447

A:Molecule type: mRNA

A:Residues: 1-495 <LAM>

A:Cross-references: UNIPROT:P27572; UNIPARC:UPI00001720FA; EMBL:X57163

A>Note: the authors translated the codon CGT for residue 418 as Ala

A:Accession: S16448

A:Molecule type: DNA

A:Residues: 1-14,'P',16-24,'TP',27-35,'P',37-51,'PP',54,'PR',57-65,'S',67-105,'S',107-12

'H',474-477,'P',479-495 <LAF>

A:Cross-references: UNIPARC:UPI000013079C; EMBL:X57164; NID:G21823; PIDN:CAA40453.1; PIC

A>Note: the authors translated the codon CGT for residue 418 as Ala

A>Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 53-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, 1

re due to RNA editing

R:Lamattina, L.; Weil, J.H.; Grienemberger, J.M.

FEBS Lett. 258, 79-83, 1989

A:Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcript

A:Reference number: S06835; MUID:90076495; PMID:2687023

A:Accession: S06835

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 295-346 <LAW>

A:Cross-references: UNIPARC:UPI00001720FB

C:Genetics:

A:Gene: nad4

A:Genome: mitochondrion

A:Introns: 154/2; 326/1; 467/1

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.8%; Score 94; DB 1; Length 495;

Best Local Similarity 24.1%; Pred. No. 1.7;

Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;

Qy 8 LSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYTLSAIAIYTSLTTLRQID--LKKIIAYSSVAHMNLVTIGMFSLNIQGI 331  
Qy 63 -----AAVLCIATIYRYKQ-----VHALSPEENVIIKLNKAGLV 98  
Db 332 GGSILLMLSHGLVSSALFLCVGLYDRHKTRLVRYYGVLVSTMPNFSTIFFFTLANMSL 391  
Qy 99 -GILSCLG--LSIVANFQKTLTFAAHVSGAVLTFPGMSLYMFVQTILSYQMOP----- 148  
Db 392 PGTSSFIGEFILVGAFORNSLVATLRALGMILGAAYSLLWLY-NRVVSGNLKPDFLYKFS 450  
Qy 149 KIHGKQVFWIR--LLLVIWCGVSALSMLTC-----SSVLHSGNF 185  
Db 451 DLNGREVFIPLFVLGVVMGVYPKVFLDCMHTSVSNLVQHGF 494  
RESULT 9  
D96506  
hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: D96506  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D96506  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-379 <STO>  
A:Cross-references: UNIPROT:Q9LPP6; UNIPARC:UPI000000BFD0; GB:AE005173; NID:g8655985; PI  
C:Genetics:  
A:Gene: T12C22.2  
A:Map position: 1  
C:Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70  
Query Match 6.7%; Score 93.5; DB 2; Length 379;  
Best Local Similarity 21.8%; Pred. No. 1.4;  
Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;  
Qy 10 FLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64  
Db 90 YIP--LLLLPSSASVESSESSCLKYI--VLIYVLLGVIIAGDNMLYSVGLLYLSASTYS 145  
Qy 65 VLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLILSCLGLSIVANFQKTLTFAAHVSG 124  
Db 146 LICATQLAFNAVFSYFINAQKFTALILNSVLLSFSAAIALNDDADTPSGVSRKYIVG 205  
Qy 125 AVLTFCGMSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGN 184  
Db 206 FVCTLAASALYSLLLSLMQFSFE-KILKRETFSVLEMQIYTSLVA----TCVSVI--GL 258  
Qy 185 FGTDLEQKLHWNPE--DKG---VYLHMITTAEWSM 215  
Db 259 FASGEWRTLHGEMEGYHKQASVYVTLVWTAVTWQV 294  
RESULT 10  
F71651  
putrescine-ornithine antiporter (potE) RP483 - Rickettsia prowazekii  
C:Species: Rickettsia prowazekii  
C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 05-Oct-2004  
C:Accession: F71651  
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U  
Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893  
A:Accession: F71651  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-429 <AND>  
A:Cross-references: UNIPROT:Q9ZD63; UNIPARC:UPI000000D37BE; GB:AJ235272; GB:AJ235269; NID  
A:Experimental source: strain Madrid E  
C:Genetics:  
A:Gene: potE; RP483  
C:Superfamily: ecotropic retrovirus receptor protein  
Query Match 6.7%; Score 93.5; DB 2; Length 429;  
Best Local Similarity 24.1%; Pred. No. 1.6;  
Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;  
Qy 11 LPSALVIWTSAAAFISYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGAMLN-- 61  
Db 217 IPRAIIIGTCCVAFLYIINSIGIIGLIPASELINSKAPY-ADAATL-----LFGGTWSKV 270  
Qy 62 ---IAAVLCIATI---YVRYKQVHALSPEENVIIKL-----NKAGLVGLILSCLGLSIV 109  
Db 271 ITVIASVICIGTLNAWVLTSGQIALGLAEDGLLPKFFAKKNSNNAPTYGIIISCLGITPL 330  
Qy 110 ANFOKTTLFAAHVSGAVLTFPGMSLYMFVQTILSYQMOPKI-HGKQVFWIRLLLVIWCGV 168  
Db 331 LLFTSNNFKAQIT-QIIDFSV-IAFLFVYLICSLAFLKVFSSKENFSYYLFF-----V 383  
Qy 169 SALSMLTCSSVLHSGNFGT 187  
Db 384 AIISIIFCTWWIYKTPPET 402  
RESULT 11  
F90693  
mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrai  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: F90693  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: F90693  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1120 <HAY>  
A:Cross-references: UNIPROT:Q8XD54; UNIPARC:UPI000000D03CB; GB:BA000007; PIDN:BAB33941.1;  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs0518  
Query Match 6.7%; Score 93; DB 2; Length 1120;  
Best Local Similarity 19.6%; Pred. No. 5;  
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;  
Qy 1 MWWFQQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
Db 805 MFW-----AIWSDLITVFSYLDISITLWHYNG-----TEAGAAVVKNVMTMGSL 847  
Qy 61 -----NIAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLS- 102  
Db 848 FAIIASMVAWALIRNLPGLLEVLSRLNMRQGASVYAITTILNYIIIAVGAMTVFGSLGV 907  
Qy 103 -----CLGLSIVANFQKTLTFAAHVSGAVLTF-----GMGSLYMF 137  
Db 908 SWDKLQWLAAALSVDGLGFLQEIIFGNFVSGLIILFERPVRIGDTVTIGSFSGTVSKIR 967  
Qy 138 VQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSG-NFGTDLEQ 191  
Db 968 ATTITDFDRKEVIIPNKAF-VTERLINW----SLTDTTTLRLVIRLGVAYGSDLEK 1017



Job time : 59 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: August 28, 2006, 17:31:24 ; Search time 300 Seconds  
(without alignments)  
820.180 Million cell updates/sec

Title: US-10-006-867-2  
Perfect score: 1392  
Sequence: 1 MWFFQQGLSFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1392	100.0	266	2	Q6UX65 HUMAN
2	1383	99.4	266	2	Q4VWF6 HUMAN
3	1295	93.0	266	2	Q3ZC48 BOVIN
4	1245	89.4	267	2	Q9CR48 MOUSE
5	1236	88.8	267	2	Q5BK09 RAT
6	1235	88.7	267	2	Q9D520 MOUSE
7	805.5	57.9	180	2	Q9D835 MOUSE
8	764.5	54.9	272	2	Q6IQI0 BRARE
9	725	52.1	136	2	Q8NBQ4 HUMAN
10	492.5	35.4	238	2	Q8N682 HUMAN
11	479.5	34.4	238	2	Q9DC58 MOUSE
12	477.5	34.3	240	2	Q5XJL0 BRARE
13	476.5	34.2	240	2	Q5RGJ7 BRARE
14	473.5	34.0	239	2	Q5EAK8 XENLA
15	471.5	33.9	287	2	Q6NRS6 XENLA
16	439.5	31.6	238	2	Q8QGB2 ONCMY
17	388.5	27.9	237	2	Q7QE61 ANOGA
18	361.5	26.0	246	2	Q77262 DROME
19	332.5	23.9	267	2	Q5DAX3 SCHJA
20	318.5	22.9	252	2	Q86F93 SCHJA
21	289.5	20.8	232	2	Q32PK2 BRARE
22	288	20.7	271	2	Q93319 CAEEL
23	277	19.9	73	2	Q4T6B8 TETNG
24	267.5	19.2	231	2	Q4V7T3 XENLA
25	262	18.8	238	2	Q8R218 MOUSE
26	260	18.7	293	2	Q61P61 CAEBR
27	258.5	18.6	230	2	Q4V7T7 XENLA
28	251.5	18.1	181	2	Q6XHF5 DROYA
29	251	18.0	132	2	Q9NUN1 HUMAN
30	248	17.8	257	2	Q5DGL6 SCHJA
31	247	17.7	132	2	Q5EA39 BOVIN

32	240	17.2	132	2	Q78J26_MOUSE	Q78j26	mus musculu
33	203	14.6	249	2	Q8C8S3_MOUSE	Q8c8s3	mus musculu
34	201.5	14.5	271	2	Q6GPL4_XENLA	Q6gpl4	xenopus lae
35	191.5	13.8	257	2	Q6IQJ3_BRARE	Q6iqj3	brachydanio
36	188.5	13.5	308	2	Q4SA40_TETNG	Q4sa40	tetraodon n
37	185.5	13.3	219	2	Q6P6P1_MOUSE	Q6p6p1	mus musculu
38	183.5	13.2	294	2	Q7SXX4_BRARE	Q7sxx4	brachydanio
39	174.5	12.5	243	2	Q559G4_DICDI	Q559g4	dictyosteli
40	172.5	12.4	243	2	Q86IK0_DICDI	Q86ik0	dictyosteli
41	161.5	11.6	123	2	Q8C9L9_MOUSE	Q8c9l9	mus musculu
42	160.5	11.5	271	2	Q86TG1_HUMAN	Q86tg1	homo sapien
43	157.5	11.3	271	2	Q9QZE9_RAT	Q9qze9	rattus norv
44	153.5	11.0	760	2	Q4SKZ5_TETNG	Q4skz5	tetraodon n
45	151.5	10.9	271	2	Q91WN2_MOUSE	Q91wn2	mus musculu
46	150.5	10.8	243	2	Q86K17_DICDI	Q86k17	dictyosteli
47	147.5	10.6	251	2	Q556P1_DICDI	Q556p1	dictyosteli
48	133.5	9.6	233	2	Q4T6B7_TETNG	Q4t6b7	tetraodon n
49	125.5	9.0	147	2	Q3TL78_MOUSE	Q3tl78	mus musculu
50	121.5	8.7	241	2	Q23135_CAEEL	Q23135	caenorhabdi
51	120.5	8.7	207	2	Q550K4_DICDI	Q550k4	dictyosteli
52	119.5	8.6	273	2	Q628C5_CAEBR	Q628c5	caenorhabdi
53	117.5	8.4	246	2	Q61US8_CAEBR	Q61us8	caenorhabdi
54	113	8.1	362	2	Q3S118_RALME	Q3s118	ralstonia m
55	112.5	8.1	252	2	Q9U3J7_CAEEL	Q9u3j7	caenorhabdi
56	112	8.0	307	2	Q474C6_RALEJ	Q474c6	ralstonia e
57	110.5	7.9	193	2	Q5C7G1_SCHJA	Q5c7g1	schistosoma
58	107.5	7.7	435	2	Q7QJU9_ANOGA	Q7qju9	anopheles g
59	106.5	7.7	140	2	Q8K117_MOUSE	Q8k117	mus musculu
60	105.5	7.6	207	2	Q54KE7_DICDI	Q54ke7	dictyosteli
61	105.5	7.6	881	2	Q5HAJ2_EHRRW	Q5haj2	ehrlichia r
62	105	7.5	217	2	Q5NE86_FRATT	Q5ne86	francisella
63	104.5	7.5	229	2	Q2WMT5_CLOBE	Q2wmt5	clostridium
64	103	7.4	299	2	Q6CDS5_YARLI	Q6cds5	yarrowia li
65	103	7.4	332	1	HMEC_ARCFU	Q29749	archaeoglob
66	103	7.4	643	2	Q55RS8_CRYNE	Q55rs8	cryptococcu
67	103	7.4	643	2	Q5KG81_CRYNE	Q5kg81	cryptococcu
68	101.5	7.3	255	2	Q9VPT7_DROME	Q9vpt7	drosophila
69	101.5	7.3	332	2	Q650W2_ORYSA	Q650w2	oryza sativ
70	101.5	7.3	881	2	Q5FG25_EHRRG	Q5fg25	ehrlichia r
71	101	7.3	218	2	Q8N2R6_HUMAN	Q8n2r6	homo sapien
72	101	7.3	293	2	Q65RP9_MANSM	Q65rp9	mannheimia
73	101	7.3	495	1	NU4M_ARATH	P93313	arabidopsis
74	101	7.3	539	2	Q8EJE2_SHEON	Q8eje2	shewanella
75	100	7.2	347	2	Q46F94_METBA	Q46f94	methanosarc
76	99	7.1	305	2	Q3YR32_EHRCJ	Q3yr32	ehrlichia c
77	98.5	7.1	456	2	Q6D428_ERWCT	Q6d428	erwinia car
78	98.5	7.1	1120	2	Q5PFL4_SALPA	Q5pfl4	salmonella
79	98.5	7.1	1120	2	Q8ZRA5_SALTY	Q8zra5	salmonella
80	98.5	7.1	1120	2	Q8Z8T6_SALTI	Q8z8t6	salmonella
81	98.5	7.1	1140	2	Q57S86_SALCH	Q57s86	salmonella
82	98	7.0	495	2	Q6YSN0_BRANA	Q6ysn0	brassica na
83	98	7.0	495	2	Q8M8A9_BETVU	Q8m8a9	beta vulgar
84	97.5	7.0	664	2	Q966D8_CAEEL	Q966d8	caenorhabdi
85	97.5	7.0	746	2	Q9N5Q9_CAEEL	Q9n5q9	caenorhabdi
86	97	7.0	382	2	Q38ZL6_LACSS	Q38zl6	lactobacill
87	97	7.0	390	2	Q8XQM0_RALSO	Q8xqm0	ralstonia s
88	97	7.0	604	2	Q9Y9X7_AERPE	Q9y9x7	aeropyrum p
89	96.5	6.9	608	2	Q4HX42_GIBZE	Q4hx42	gibberella
90	96	6.9	369	2	Q38YX3_LACSS	Q38yx3	lactobacill
91	96	6.9	395	2	Q8EFB8_SHEON	Q8efb8	shewanella
92	96	6.9	460	2	Q3A8B8_PELCD	Q3a8b8	pelobacter
93	96	6.9	495	2	Q37544_LACSA	Q37544	lactuca sat
94	96	6.9	535	2	Q2ZBK9_9GAMM	Q2zbk9	shewanella
95	96	6.9	535	2	Q363W2_9GAMM	Q363w2	shewanella
96	96	6.9	535	2	Q36HJ6_9GAMM	Q36hj6	shewanella
97	96	6.9	572	2	Q4BVX0_CROWT	Q4bvxo	crocospaer
98	96	6.9	615	2	Q7S1C6_NEUCR	Q7s1c6	neurospora
99	95.5	6.9	268	2	Q5WSU3_LEGPL	Q5wsu3	legionella
100	95.5	6.9	284	2	Q4ZWZ1_PSEU2	Q4zwz1	pseudomonas
101	95.5	6.9	291	2	Q9ZFP3_ENTFC	Q9zfp3	enterococcu
102	95.5	6.9	309	2	Q6NRD6_XENLA	Q6nrd6	xenopus lae
103	95.5	6.9	388	2	Q4PDK8_USTMA	Q4pdk8	ustilago ma
104	95.5	6.9	486	2	Q8FQF5_COREF	Q8fqf5	corynebacte

105	95	6.8	440	2	Q4WU03_ASPPU	Q4wu03 aspergillus	178	90.5	6.5	614	2	Q9LNF0_ARATH	Q9lnf0 arabidopsis
106	95	6.8	699	2	Q38VM9_LACSS	Q38vm9 lactobacill	179	90.5	6.5	814	2	Q2ZY24_STRSU	Q2zy24 streptococc
107	95	6.8	702	2	Q9SC10_9MAGN	Q9sc10 tetracera a	180	90.5	6.5	1505	2	Q73JH5_TREDE	Q73jh5 treponema d
108	95	6.8	1120	2	Q325D1_SHIDS	Q325d1 shigella bo	181	90	6.5	281	2	Q54J51_DICDI	Q54j51 dictyosteli
109	94.5	6.8	229	2	Q4RRI4_TETNG	Q4rri4 tetraodon n	182	90	6.5	283	2	Q8NUB1_CORGL	Q8nub1 corynebacte
110	94.5	6.8	268	2	Q5X117_LEGPA	Q5x117 legionella	183	90	6.5	396	2	Q8FFS3_ECOL6	Q8ffs3 escherichia
111	94.5	6.8	463	2	Q41CA9_9BACI	Q41ca9 exigubacte	184	90	6.5	400	2	Q9KN80_VIBCH	Q9kn80 vibrio chol
112	94.5	6.8	469	2	Q7UF66_RHOBA	Q7uf66 rhodopirell	185	90	6.5	458	2	Q4S023_TETNG	Q4s023 tetraodon n
113	94.5	6.8	724	2	Q6FU10_CANGA	Q6ful0 candida gla	186	90	6.5	492	1	NU4M_CHOCR	P48915 chondrus cr
114	94	6.8	266	2	Q4FWG7_LEIMA	Q4fwg7 leishmania	187	90	6.5	498	2	Q40PE9_DESAC	Q40pe9 desulfuromo
115	94	6.8	283	2	Q88MV8_PSEPK	Q88mv8 pseudomonas	188	90	6.5	505	2	Q5AEG5_CANAL	Q5aeg5 candida alb
116	94	6.8	452	2	Q5FI09_LACAC	Q5fi09 lactobacill	189	90	6.5	528	1	ATG22_YEAST	P25568 saccharomyc
117	94	6.8	495	1	NU4M_WHEAT	P27572 triticum ae	190	90	6.5	554	2	Q8GJF7_DDEBA	Q8gjf7 bdellovibri
118	94	6.8	542	2	Q3Q8S5_9GAMM	Q3q8s5 shewanella	191	90	6.5	557	2	Q877D2_9CREN	Q877d2 pyrobaculum
119	94	6.8	543	2	Q3NTZ4_SHEFR	Q3ntz4 shewanella	192	90	6.5	669	2	Q5A3N6_CANAL	Q5a3n6 candida alb
120	94	6.8	820	2	Q61KL4_CAEBR	Q61kl4 caenorhabdi	193	90	6.5	669	2	Q5A3V1_CANAL	Q5a3v1 candida alb
121	94	6.8	1120	2	Q8FK90_ECOL6	Q8fk90 escherichia	194	90	6.5	739	2	Q6MKW0_DDEBA	Q6mkw0 bdellovibri
122	93.5	6.7	303	2	Q2V4I7_ARATH	Q2v4i7 arabidopsis	195	89.5	6.4	270	2	Q886V4_PSESM	Q886v4 pseudomonas
123	93.5	6.7	367	2	Q3E7M0_ARATH	Q3e7m0 arabidopsis	196	89.5	6.4	360	2	Q30PV3_THIDN	Q30pv3 thiomicrosp
124	93.5	6.7	379	2	Q9LPF6_ARATH	Q9lpf6 arabidopsis	197	89.5	6.4	375	2	Q3CZL3_STRAG	Q3czl3 streptococc
125	93.5	6.7	429	2	Q9ZD63_RICPR	Q9zd63 rickettsia	198	89.5	6.4	437	2	Q9CLI4_PASMU	Q9cll4 pasteurella
126	93.5	6.7	440	2	Q4QMF2_HAEI8	Q4qmf2 haemophilus	199	89.5	6.4	440	1	DCUB_HAEIN	P44855 haemophilus
127	93.5	6.7	680	2	Q3G8W9_9FIRM	Q3g8w9 syntrophomo	200	89.5	6.4	440	2	Q65QD7_MANSM	Q65qd7 mannheimia
128	93.5	6.7	1624	2	Q4I335_GIBZE	Q4i335 gibberella	201	89.5	6.4	443	2	Q929T2_LISIN	Q929t2 listeria in
129	93	6.7	576	2	Q5ZSX8_LEGPH	Q5zxs8 legionella	202	89.5	6.4	445	2	Q41ZY6_DESHA	Q41zy6 desulfitoba
130	93	6.7	688	2	Q34CS1_RHOPA	Q34cs1 rhodopseudo	203	89.5	6.4	473	2	Q57LZ5_SALCH	Q57lz5 salmonella
131	93	6.7	797	2	Q45585_CAEEL	Q45585 caenorhabdi	204	89.5	6.4	482	2	Q4VIG2_BACCH	Q4vlg2 bacillus ce
132	93	6.7	1120	1	KEFA_ECOLI	P77338 escherichia	205	89.5	6.4	485	2	Q88T41_LACPL	Q88t41 lactobacill
133	93	6.7	1120	2	Q32J45_SHIDS	Q32j45 shigella dy	206	89.5	6.4	495	2	O59121_PYRHO	O59121 pyrococcus
134	93	6.7	1120	2	Q3Z4T4_SHISS	Q3z4t4 shigella so	207	89.5	6.4	511	2	Q44R91_CHLLI	Q44r91 chlorobium
135	93	6.7	1120	2	Q2MBW2_ECOLI	Q2mbw2 escherichia	208	89.5	6.4	521	2	O5ZYV3_LEGPH	O5zyv3 legionella
136	93	6.7	1120	2	Q8XD54_ECO57	Q8xd54 escherichia	209	89.5	6.4	527	2	Q35I37_9BRAD	Q35i37 bradyrhizob
137	93	6.7	1120	2	Q83SE8_SHIFL	Q83se8 shigella fl	210	89.5	6.4	579	2	Q3DAC9_STRAG	Q3dac9 streptococc
138	93	6.7	1264	2	Q6BT03_DEBHA	Q6bt03 debaryomyce	211	89.5	6.4	579	2	Q3DHF4_STRAG	Q3dhf4 streptococc
139	92.5	6.6	251	2	Q970A1_SULTO	Q970a1 sulfolobus	212	89.5	6.4	579	2	Q3DTN1_STRAG	Q3dtn1 streptococc
140	92.5	6.6	473	2	Q8ZNC5_SALTY	Q8znc5 salmonella	213	89.5	6.4	579	2	Q3K170_STRAL	Q3k170 streptococc
141	92.5	6.6	473	2	Q8Z506_SALTI	Q8z506 salmonella	214	89.5	6.4	579	2	Q8DZT0_STRAS	Q8dzt0 streptococc
142	92.5	6.6	479	2	Q6SGM5_9BACT	Q6sgm5 uncultured	215	89.5	6.4	579	2	Q8E5H7_STRAS	Q8e5h7 streptococc
143	92.5	6.6	538	2	Q33WQ9_9GAMM	Q33wq9 shewanella	216	89.5	6.4	599	2	Q22089_CAEEL	Q22089 caenorhabdi
144	92.5	6.6	634	2	Q5KSP7_9ECHI	Q5ksp7 astropecten	217	89.5	6.4	963	2	Q7R2T8_GIALA	Q7r2t8 giardia lam
145	92.5	6.6	977	2	Q6CK54_KLULA	Q6ck54 kluyveromyc	218	89.5	6.4	1132	2	Q3NPV4_SHEFR	Q3npv4 shewanella
146	92.5	6.6	1117	2	Q4KJF2_PSEF5	Q4kjf2 pseudomonas	219	89	6.4	267	2	Q8BV59_MOUSE	Q8bv59 mus musculu
147	92	6.6	399	2	Q3P0W7_9GAMM	Q3p0w7 shewanella	220	89	6.4	290	2	Q812M6_BACCR	Q812m6 bacillus ce
148	92	6.6	434	2	Q7VN68_HAEDU	Q7vn68 haemophilus	221	89	6.4	290	2	Q72YR6_BACC1	Q72yr6 bacillus ce
149	92	6.6	449	2	Q2JYC6_RHIET	Q2jyc6 rhizobium e	222	89	6.4	293	2	Q377V6_RHOPA	Q377v6 rhodopseudo
150	92	6.6	454	2	Q51J37_ENTHI	Q5i3q7 entamoeba h	223	89	6.4	318	2	Q3G9U1_9FIRM	Q3g9u1 syntrophomo
151	92	6.6	594	2	Q5V2N6_HALMA	Q5v2n6 haloarcula	224	89	6.4	360	2	Q2XDW3_PSEPU	Q2xdw3 pseudomonas
152	91.5	6.6	268	2	Q5ZRL1_LEGPH	Q5zrl1 legionella	225	89	6.4	428	2	Q66FK2_YERPS	Q66fk2 yersinia ps
153	91.5	6.6	279	2	Q3Y299_ENTFC	Q3y299 enterococcu	226	89	6.4	428	2	Q8ZJ45_YERPE	Q8zj45 yersinia pe
154	91.5	6.6	387	2	Q22188_CAEEL	Q22188 caenorhabdi	227	89	6.4	442	2	Q7MP35_VIBVY	Q7mp35 vibrio vuln
155	91.5	6.6	430	2	Q8I0L4_CAEEL	Q8i0l4 caenorhabdi	228	89	6.4	637	2	Q9H8H9_HUMAN	Q9h8h9 homo sapien
156	91.5	6.6	444	2	Q67EN8_CALSI	Q67en8 callinectes	229	89	6.4	659	2	Q7VUY3_BORPE	Q7vuy3 bordetella
157	91.5	6.6	447	2	Q5QZ24_IDILO	Q5qz24 idiomarina	230	89	6.4	660	2	Q7WBD6_BORPA	Q7wbd6 bordetella
158	91.5	6.6	477	2	Q5U6C1_BETVU	Q5u6c1 beta vulgar	231	89	6.4	757	2	Q9UFA2_HUMAN	Q9ufa2 homo sapien
159	91.5	6.6	495	2	Q9MF62_BETVU	Q9mf62 beta vulgar	232	89	6.4	917	2	Q9H698_HUMAN	Q9h698 homo sapien
160	91.5	6.6	530	2	Q88W48_LACPL	Q88w48 lactobacill	233	89	6.4	1011	2	Q96F81_HUMAN	Q96f81 homo sapien
161	91.5	6.6	712	1	POT1_ARATH	Q22397 arabidopsis	234	88.5	6.4	252	2	Q384Q8_9TRYP	Q384q8 trypanosoma
162	91.5	6.6	712	2	Q56YD6_ARATH	Q56yd6 arabidopsis	235	88.5	6.4	266	2	Q4IXM4_AZOV1	Q4ixm4 azotobacter
163	91.5	6.6	732	2	Q9TJY8_9GENT	Q9tjy8 condaminea	236	88.5	6.4	279	2	Q4BVQ2_CROWT	Q4bvq2 crocosphaer
164	91.5	6.6	793	2	Q3S1J3_THIDA	Q3s1j3 thiobacillu	237	88.5	6.4	283	2	Q43QV3_SOLUS	Q43qv3 solibacter
165	91.5	6.6	1085	2	Q7VQP9_BLOFL	Q7vqp9 blochmannia	238	88.5	6.4	361	1	MRAY_COXBU	Q83f26 coxiella bu
166	91.5	6.6	1117	2	Q3KJ67_PSEPF	Q3kj67 pseudomonas	239	88.5	6.4	361	1	MRAY_LEGPA	Q5x183 legionella
167	91.5	6.6	1221	2	Q4Q6N2_LEIMA	Q4q6n2 leishmania	240	88.5	6.4	403	2	Q55XU0_CRYNE	Q55xu0 cryptococcu
168	91	6.5	257	2	Q6HIW4_BACHK	Q6hiw4 bacillus th	241	88.5	6.4	403	2	Q5KM52_CRYNE	Q5km52 cryptococcu
169	91	6.5	262	2	Q4WC47_ASPPU	Q4wc47 aspergillus	242	88.5	6.4	430	2	Q9V210_PYRAB	Q9v210 pyrococcus
170	91	6.5	340	2	Q5NLJ5_ZYMMO	Q5nlj5 zymomonas m	243	88.5	6.4	672	2	Q2MV24_9CHLO	Q2mv24 dunaliella
171	91	6.5	372	2	Q8NXX5_STAAR	Q8nxe5 staphylococ	244	88.5	6.4	680	2	Q9SBY7_9ASTE	Q9sby7 vahlia cape
172	91	6.5	552	2	Q7WNJ3_BORBR	Q7wnj3 bordetella	245	88.5	6.4	685	2	Q2S0C0_9SPHI	Q2s0c0 salinibacte
173	91	6.5	554	2	Q37EY9_RHOPA	Q37ey9 rhodopseudo	246	88.5	6.4	691	2	Q8M8V0_9ASTE	Q8m8v0 vahlia cape
174	90.5	6.5	311	2	Q6CLU8_KLULA	Q6clu8 kluyveromyc	247	88.5	6.4	732	2	Q9TJP3_9GENT	Q9tjp3 simira viri
175	90.5	6.5	337	2	Q4NLG6_9MICC	Q4nlg6 arthrobacte	248	88.5	6.4	732	2	Q9TJS2_9GENT	Q9tjs2 pentagonia
176	90.5	6.5	443	2	Q5JH08_PYRKO	Q5jh08 pyrococcus	249	88.5	6.4	807	2	Q5CZ47_CAEEL	Q5cz47 caenorhabdi
177	90.5	6.5	579	2	Q3DLK9_STRAG	Q3dlk9 streptococc	250	88.5	6.4	808	2	Q21453_CAEEL	Q21453 caenorhabdi

251	88.5	6.4	833	2	Q7USM4_RHOBA	Q7usm4 rhodopirell	324	87	6.2	596	2	Q43WI9_SOLUS	Q43wi9 solibacter
252	88.5	6.4	1057	2	Q3PVW1_NITHA	Q3pvw1 nitrobacter	325	87	6.2	613	2	Q9I4D1_PSEAB	Q9i4d1 pseudomonas
253	88	6.3	263	2	Q3A731_PELCD	Q3a731 pelobacter	326	87	6.2	928	2	Q9LEC9_SOLFU	Q9lec9 solanum tub
254	88	6.3	290	2	Q4MVA6_BACCE	Q4mva6 bacillus ce	327	86.5	6.2	261	2	Q4QLK2_HAEI8	Q4qlk2 haemophilus
255	88	6.3	290	2	Q632P0_BACCC	Q632p0 bacillus ce	328	86.5	6.2	301	2	Q970T4_SULTO	Q970t4 sulfolobus
256	88	6.3	290	2	Q6HC79_BACHK	Q6hc79 bacillus th	329	86.5	6.2	341	2	Q44MQ7_CHLLI	Q44mq7 chlorobium
257	88	6.3	290	2	Q81KE4_BACAN	Q81ke4 bacillus an	330	86.5	6.2	368	2	Q839R1_ENTFA	Q839r1 enterococcu
258	88	6.3	324	2	Q4SF91_TETNG	Q4sf91 tetraodon n	331	86.5	6.2	400	1	YCEI_BACSU	Q34691 bacillus su
259	88	6.3	331	2	Q2RKU5_MOOTH	Q2rku5 moorella th	332	86.5	6.2	403	2	Q4WDR2_ASPPU	Q4wdr2 aspergillus
260	88	6.3	372	2	Q8AIP0_BACTN	Q8aip0 bacteroides	333	86.5	6.2	441	2	Q4SY26_TETNG	Q4sy26 tetraodon n
261	88	6.3	413	2	Q8R792_THETN	Q8r792 thermoanaer	334	86.5	6.2	465	2	Q38SD3_TETNG	Q38sd3 tetraodon n
262	88	6.3	437	2	Q4ZTV4_PSEU2	Q4ztv4 pseudomonas	335	86.5	6.2	467	2	Q41QU4_FERAC	Q41qu4 ferroplasma
263	88	6.3	500	2	Q9TCC1_NEPOL	Q9tcc1 nephroselmi	336	86.5	6.2	544	2	Q4UCA2_THEAN	Q4uca2 theileria a
264	88	6.3	512	2	Q469Q3_METBA	Q469q3 methanosarc	337	86.5	6.2	547	2	Q5L797_CHLAB	Q5l797 chlamydophi
265	88	6.3	524	2	Q4NGA1_9MICC	Q4nga1 arthrobacte	338	86.5	6.2	547	2	Q6N8M3_RHOPA	Q6n8m3 rhodopseudo
266	88	6.3	530	2	Q37CM4_RHOPA	Q37cm4 rhodopseudo	339	86.5	6.2	549	2	Q4KDN8_PSEF5	Q4kdn8 pseudomonas
267	88	6.3	546	2	Q8XP0_METMA	Q8xp0 methanosarc	340	86.5	6.2	557	2	Q8ZXC1_PYRAE	Q8zxc1 pyrobaculum
268	88	6.3	622	2	Q7S317_NEUCR	Q7s317 neurospora	341	86.5	6.2	583	2	Q4ERC2_LISTER	Q4erc2 listeria mo
269	88	6.3	660	2	Q7WMV6_BORBR	Q7wmv6 bordetella	342	86.5	6.2	583	2	Q8Y9B6_LISMO	Q8y9b6 listeria mo
270	88	6.3	661	2	Q74F70_GEOSL	Q74f70 geobacter s	343	86.5	6.2	586	2	Q7ZV33_BRARE	Q7zv33 brachydanio
271	88	6.3	732	2	Q9TJP1_9GENT	Q9tjpl warszewiczi	344	86.5	6.2	659	2	Q8MGF7_9DIPS	Q8mgf7 valeriana j
272	88	6.3	787	2	Q6SHL0_9BACT	Q6shl0 uncultured	345	86.5	6.2	732	2	Q9TJV8_9GENT	Q9tjv8 chimarrhis
273	88	6.3	929	2	Q9LGC6_ORYSA	Q9lgc6 oryza sativ	346	86.5	6.2	770	2	Q9YCS4_AERPE	Q9ycs4 aeropyrum p
274	88	6.3	1165	1	ADCY6_CANFA	P30804 canis famil	347	86.5	6.2	1527	2	Q4UD84_THEAN	Q4ud84 theileria a
275	87.5	6.3	215	2	Q9D2W6_MOUSE	Q9d2w6 mus musculu	348	86	6.2	198	2	Q3EZK8_BACTI	Q3ezk8 bacillus th
276	87.5	6.3	233	1	Y117_BORBU	O51144 borrelia bu	349	86	6.2	229	2	Q3PRM4_NITHA	Q3prm4 nitrobacter
277	87.5	6.3	235	2	Q5NQ68_ZYMMO	Q5nq68 zymomonas m	350	86	6.2	233	2	Q662P5_BORGA	Q662p5 borrelia ga
278	87.5	6.3	284	2	Q48LW2_PSE14	Q48lw2 pseudomonas	351	86	6.2	234	2	Q8R3W1_MOUSE	Q8r3w1 mus musculu
279	87.5	6.3	300	2	Q5OYH0_ENTHI	Q50yh0 entamoeba h	352	86	6.2	254	2	Q5DBF3_SCHJA	Q5dbf3 schistosoma
280	87.5	6.3	342	2	Q3GGZ3_CHLVI	Q3ggz3 prosthecoch	353	86	6.2	279	2	Q3NMX9_SHEFR	Q3nmx9 shewanella
281	87.5	6.3	361	1	MRAY_LEGPH	Q5zsa2 legionella	354	86	6.2	331	2	Q3GHP3_CHLVI	Q3ghp3 prosthecoch
282	87.5	6.3	361	1	MRAY_LEGPL	Q5wti4 legionella	355	86	6.2	339	2	Q4IEC2_GIBZE	Q4iec2 gibberella
283	87.5	6.3	365	2	Q6KHR7_MYCMO	Q6khr7 mycoplasma.	356	86	6.2	372	2	Q5HHA6_STAAC	Q5hha6 staphylococ
284	87.5	6.3	374	2	Q3FU92_9BURK	Q3fu92 rhodoferrax	357	86	6.2	372	2	Q6GAU7_STAAS	Q6gau7 staphylococ
285	87.5	6.3	427	2	Q4UL81_RICFE	Q4ul81 rickettsia	358	86	6.2	373	2	Q7A6G2_STAAN	Q7a6g2 staphylococ
286	87.5	6.3	429	2	Q68WP9_RICTY	Q68wp9 rickettsia	359	86	6.2	373	2	Q99VB1_STAAM	Q99vb1 staphylococ
287	87.5	6.3	429	2	Q9KRP3_VIBCH	Q9krp3 vibrio chol	360	86	6.2	389	2	Q9V0C0_PYRAB	Q9v0c0 pyrococcus
288	87.5	6.3	453	1	SERC1_MOUSE	Q9qzi8 mus musculu	361	86	6.2	396	1	BCR_ECOLI	P28246 escherichia
289	87.5	6.3	453	2	Q642W5_9ANNE	Q642w5 clymenella	362	86	6.2	396	2	Q2MAQ9_ECOLI	Q2maq9 escherichia
290	87.5	6.3	453	2	Q3UZ93_MOUSE	Q3uz93 m 8 days em	363	86	6.2	396	2	Q32HY2_SHIDS	Q32hy2 shigella dy
291	87.5	6.3	453	2	Q7TNK0_RAT	Q7tnk0 rattus norv	364	86	6.2	444	2	Q7Y8W4_9EUCA	Q7y8w4 portunus tr
292	87.5	6.3	456	2	Q6BQ78_DEBHA	Q6bq78 debaryomyce	365	86	6.2	494	2	Q36BY3_9GAMM	Q36by3 shewanella
293	87.5	6.3	473	2	Q5PN23_SALPA	Q5pn23 salmonella	366	86	6.2	509	2	Q7R5J8_GIALA	Q7r5j8 giardia lam
294	87.5	6.3	482	1	YFIG_BACSU	P54723 bacillus su	367	86	6.2	531	2	Q2IUB9_RHOPA	Q2iub9 rhodopseudo
295	87.5	6.3	521	2	Q5X8G4_LEGPA	Q5x8g4 legionella	368	86	6.2	593	2	Q2JTV5_9CYAN	Q2jtv5 cyanobacter
296	87.5	6.3	530	2	Q8EMR7_OCEIH	Q8emr7 oceanobacil	369	86	6.2	667	2	Q8W9Q3_MESVI	Q8w9q3 mesostigma
297	87.5	6.3	544	2	Q18061_CAEEL	O18061 caenorhabdi	370	86	6.2	701	2	Q8HTM4_ACHTR	Q8htm4 achlys trip
298	87.5	6.3	547	2	Q824X5_CHLCV	Q824x5 chlamydophi	371	86	6.2	703	2	Q9LMM3_ARATH	Q9lmm3 arabidopsis
299	87.5	6.3	671	2	Q73WX6_MYCPA	Q73wx6 mycobacteri	372	86	6.2	725	2	P92949_ARATH	P92949 arabidopsis
300	87.5	6.3	732	2	Q9TJQ2_9GENT	Q9tjq2 rustia sple	373	86	6.2	841	1	MPRF_STAXY	Q93qy7 staphylococ
301	87.5	6.3	737	2	Q7Q8T7_ANOGA	Q7q8t7 anopheles g	374	86	6.2	883	2	Q3YRC6_EHRCJ	Q3yrc6 ehrlichia c
302	87.5	6.3	833	2	Q4JSU6_CORJK	Q4jsu6 corynebacte	375	86	6.2	954	2	Q7VGA9_HELHP	Q7vga9 helicobacte
303	87.5	6.3	1687	2	Q6QL17_RAT	Q6qil7 rattus norv	376	86	6.2	1308	2	Q8T6H2_DICDI	Q8t6h2 dictyosteli
304	87	6.2	161	2	Q4S8L4_TETNG	Q4s8l4 tetraodon n	377	86	6.2	1328	2	Q54EK2_DICDI	Q54ek2 dictyosteli
305	87	6.2	257	2	Q4V0X1_BACCC	Q4v0x1 bacillus ce	378	86	6.2	1463	2	Q5AVK4_EMENI	Q5avk4 aspergillus
306	87	6.2	261	2	Q7VLV2_HAEDU	Q7vlv2 haemophilus	379	85.5	6.1	219	2	Q9CY24_MOUSE	Q9cy24 mus musculu
307	87	6.2	269	2	Q458S9_9BURK	Q458s9 burkholderi	380	85.5	6.1	219	2	Q9D8L7_MOUSE	Q9d8l7 mus musculu
308	87	6.2	269	2	Q4LR84_9BURK	Q4lr84 burkholderi	381	85.5	6.1	250	2	Q6CID8_KLJLA	Q6cid8 kluyveromyc
309	87	6.2	271	2	Q6FFL1_ACIAI	Q6ffl1 acinetobact	382	85.5	6.1	261	2	Q9CP79_PASMU	Q9cp79 pasteurella
310	87	6.2	350	2	Q3H352_9ACTO	Q3h352 nocardioide	383	85.5	6.1	295	2	Q9K0I7_NEIMB	Q9k0i7 neisseria m
311	87	6.2	396	2	Q8X5A2_ECO57	Q8x5a2 escherichia	384	85.5	6.1	295	2	Q5FA38_NEIG1	Q5fa38 neisseria g
312	87	6.2	410	2	Q62BS8_BURMA	Q62bs8 burkholderi	385	85.5	6.1	296	2	Q669X3_YERPE	Q669x3 yersinia ps
313	87	6.2	410	2	Q63LL0_BURPS	Q63ll0 burkholderi	386	85.5	6.1	296	2	Q82F11_YERPE	Q8zfi1 yersinia pe
314	87	6.2	412	2	Q4J7I0_SULAC	Q4j7i0 sulfolobus	387	85.5	6.1	304	2	Q40JK4_EHRCH	Q40jk4 ehrlichia c
315	87	6.2	418	2	Q2VHS5_9ENTR	Q2vhs5 kluyvera as	388	85.5	6.1	311	1	PAQR3_HUMAN	Q6tch7 homo sapien
316	87	6.2	435	1	EXOQ_RHIME	Q02729 rhizobium m	389	85.5	6.1	311	2	Q88TD9_LACPL	Q88td9 lactobacill
317	87	6.2	456	2	Q3F3X5_9BURK	Q3f3x5 burkholderi	390	85.5	6.1	329	2	Q96K55_HUMAN	Q96k55 homo sapien
318	87	6.2	475	2	Q3NN43_SHEFR	Q3nn43 shewanella	391	85.5	6.1	355	2	Q8TNX8_METAC	Q8tnx8 methanosarc
319	87	6.2	517	2	Q61HG9_CAEBR	Q61hg9 caenorhabdi	392	85.5	6.1	399	2	Q75PY5_CAVPO	Q75py5 cavia porce
320	87	6.2	535	2	Q5WU59_LEGPL	Q5wu59 legionella	393	85.5	6.1	401	2	Q89KV1_BRAJA	Q89kv1 bradyrhizob
321	87	6.2	535	2	Q5X2E0_LEGPA	Q5x2e0 legionella	394	85.5	6.1	414	2	Q2XJ85_PSEPU	Q2xj85 pseudomonas
322	87	6.2	580	2	Q5AVA3_EMENI	Q5ava3 aspergillus	395	85.5	6.1	440	2	Q3EGA9_ACTSC	Q3ega9 actinobacil
323	87	6.2	592	2	Q3JF87_BURP1	Q3jf87 burkholderi	396	85.5	6.1	453	2	Q5R419_PONPY	Q5r419 pongo pygma

397	85.5	6.1	453	2	Q5R4G3_PONPY	Q5r4g3 pongo pygma	470	84.5	6.1	479	2	Q651L0_ORYSA	Q651l0 oryza sativ
398	85.5	6.1	470	2	Q4T836_TETNG	Q4t836 tetraodon n	471	84.5	6.1	479	2	Q9WZ89_THEMA	Q9wz89 thermotoga
399	85.5	6.1	482	2	Q3CNC3_ALTAT	Q3cnc3 pseudoalter	472	84.5	6.1	491	2	Q18154_CAEBL	Q18154 caenorhabdi
400	85.5	6.1	482	2	Q4S4Z6_TETNG	Q4s4z6 tetraodon n	473	84.5	6.1	515	2	Q9LN48_ARATH	Q9ln48 arabidopsis
401	85.5	6.1	484	2	Q3UH23_MOUSE	Q3uh23 m 14 days p	474	84.5	6.1	562	2	Q9FL18_ARATH	Q9fli8 arabidopsis
402	85.5	6.1	496	2	Q5ZMS7_CHICK	Q5zms7 gallus gall	475	84.5	6.1	589	2	Q95ZY6_CAEBL	Q95zy6 caenorhabdi
403	85.5	6.1	497	2	Q2RZQ5_9SPHI	Q2rzq5 salinibacte	476	84.5	6.1	638	2	Q33749_ARBLI	Q33749 arabacia lix
404	85.5	6.1	498	2	Q2L287_RECAM	Q2l287 reclinomona	477	84.5	6.1	671	2	Q55T80_CRYNE	Q55t80 cryptococcu
405	85.5	6.1	521	2	Q8WUB5_HUMAN	Q8wub5 homo sapien	478	84.5	6.1	674	2	Q5KJ61_CRYPTOC	Q5kj61 cryptococcu
406	85.5	6.1	526	2	Q90X46_BRARE	Q90x46 brachydanio	479	84.5	6.1	702	2	Q9TLF1_9LAMI	Q9tlf1 lindenbergi
407	85.5	6.1	528	2	Q6A2J4_9LAMI	Q6a2j4 brandisia h	480	84.5	6.1	913	2	Q7UJI4_RHOBA	Q7uji4 rhodopirell
408	85.5	6.1	545	2	Q96JZ5_HUMAN	Q96jz5 homo sapien	481	84.5	6.1	1982	2	Q4Q897_LEIMA	Q4q897 leishmania
409	85.5	6.1	572	2	Q4XZG8_PLACH	Q4xzg8 plasmodium	482	84	6.0	172	2	Q9TA01_LAMFL	Q9ta01 lampetra fl
410	85.5	6.1	587	1	TM9S3_MOUSE	Q9et30 mus musculu	483	84	6.0	234	2	Q3UAR5_MOUSE	Q3uar5 mus musculu
411	85.5	6.1	589	1	TM9S3_HUMAN	Q9hd45 homo sapien	484	84	6.0	234	2	Q99N04_MOUSE	Q99n04 mus musculu
412	85.5	6.1	589	2	Q5TB57_HUMAN	Q5tb57 homo sapien	485	84	6.0	295	2	Q7YFS4_9HYME	Q7yfs4 neivamyrmex
413	85.5	6.1	629	2	Q571B0_MOUSE	Q571b0 mus musculu	486	84	6.0	298	2	Q48ER6_PSE14	Q48er6 pseudomonas
414	85.5	6.1	682	2	Q83C62_COXBU	Q83c62 coxiella bu	487	84	6.0	318	2	Q97NY1_STRPN	Q97ny1 streptococc
415	85.5	6.1	695	2	Q2QN15_ORYSA	Q2qnl5 oryza sativ	488	84	6.0	329	2	Q8U0A2_PYRFU	Q8u0a2 pyrococcus
416	85.5	6.1	696	2	Q9TIW8_9ASTE	Q9tiw8 phacelia ro	489	84	6.0	367	2	Q3DVG6_CHLAU	Q3dvg6 chloroflexu
417	85.5	6.1	703	2	Q9TLA5_9LAMI	Q9tla5 jasminum me	490	84	6.0	388	2	Q2KX95_BORAV	Q2kx95 bordetella
418	85.5	6.1	851	2	Q6FU89_CANGA	Q6fu89 candida gla	491	84	6.0	396	2	Q2JAA7_9ACTO	Q2jaa7 frankia sp.
419	85.5	6.1	999	2	Q93JY2_ERWCH	Q93jy2 erwinia chr	492	84	6.0	403	2	Q7MUU1_PORGI	Q7muu1 porphyromon
420	85	6.1	257	2	Q3V7U0_GEOKA	Q3v7u0 geobacillus	493	84	6.0	408	2	Q83MR3_TROWT	Q83mr3 tropheryma
421	85	6.1	304	2	Q96U46_NEUCR	Q96u46 neurospora	494	84	6.0	408	2	Q83N96_TROW8	Q83n96 tropheryma
422	85	6.1	307	2	Q6F7C6_ACIAD	Q6f7c6 acinetobact	495	84	6.0	448	2	Q5YTA9_NOCFA	Q5yta9 nocardia fa
423	85	6.1	333	2	Q6XCC9_CYPCA	Q6xcc9 cyprinus ca	496	84	6.0	459	2	Q5Z9R6_ORYSA	Q5z9r6 oryza sativ
424	85	6.1	338	1	PSTC1_MYCBO	P0a629 mycobacteri	497	84	6.0	460	2	Q59186_PYRHO	Q59186 pyrococcus
425	85	6.1	338	1	PSTC1_MYCTU	P0a628 mycobacteri	498	84	6.0	464	2	Q518J3_ENTHI	Q518j3 entamoeba h
426	85	6.1	339	2	Q5L5M5_CHLAB	Q5l5m5 chlamydophi	499	84	6.0	465	2	Q4ZYM6_PSEU2	Q4zym6 pseudomonas
427	85	6.1	355	2	Q4L476_STAHI	Q4l476 staphylococ	500	84	6.0	478	2	Q2X075_9GAMM	Q2x075 shewanella
428	85	6.1	361	1	MRAY_NITEU	Q82v86 nitrosomona	501	84	6.0	478	2	Q2ZX65_SHEPU	Q2zx65 shewanella
429	85	6.1	369	2	Q9N2T7_CAEBL	Q9n2t7 caenorhabdi	502	84	6.0	478	2	Q74F67_GEOSL	Q74f67 geobacter s
430	85	6.1	419	2	Q8NRU3_CORGL	Q8nru3 corynebacte	503	84	6.0	498	2	Q4E7G9_9RICK	Q4e7g9 wolbachia e
431	85	6.1	423	2	Q2US59_ASPOR	Q2us59 aspergillus	504	84	6.0	510	2	Q33Q28_9GAMM	Q33q28 shewanella
432	85	6.1	427	2	Q7PKH1_ANOGA	Q7pkh1 anopheles g	505	84	6.0	524	2	Q35C75_9BRAD	Q35c75 bradyrhizob
433	85	6.1	443	2	Q9CEP2_LACLA	Q9cep2 lactococcus	506	84	6.0	539	2	Q41LL5_METBU	Q41ll5 methanococc
434	85	6.1	453	1	CAX1B_ORYSA	Q5tkg3 oryza sativ	507	84	6.0	575	2	Q9I642_PSEAE	Q9i642 pseudomonas
435	85	6.1	462	2	Q96YE7_SULTO	Q96ye7 sulfolobus	508	84	6.0	587	2	Q48BL8_PSE14	Q48bl8 pseudomonas
436	85	6.1	469	2	Q4C4C5_CROWT	Q4c4c5 crocosphaer	509	84	6.0	597	2	Q9KUW6_VIBCH	Q9kuw6 vibrio chol
437	85	6.1	478	2	Q3Q3R8_9GAMM	Q3q3r8 shewanella	510	84	6.0	599	2	Q61Z28_CAEBR	Q61z28 caenorhabdi
438	85	6.1	497	2	Q6BY36_DEBHA	Q6by36 debaryomyce	511	84	6.0	602	2	Q5QS30_MACLA	Q5q830 macrotis la
439	85	6.1	498	2	Q9QXP0_MOUSE	Q9qxp0 mus musculu	512	84	6.0	673	2	Q46RW6_RALEJ	Q46rw6 ralstonia e
440	85	6.1	522	2	Q9B8X9_FASHE	Q9b8x9 fasciola he	513	84	6.0	679	2	Q511J8_ENTHI	Q511j8 entamoeba h
441	85	6.1	524	2	Q8U4T9_HALVO	Q8u4t9 halobacteri	514	84	6.0	679	2	Q518I7_ENTHI	Q518i7 entamoeba h
442	85	6.1	543	2	Q83NH2_TROW8	Q83nh2 tropheryma	515	84	6.0	736	2	Q9TJS1_9GENT	Q9tjs1 pauidianth
443	85	6.1	543	2	Q83GL8_TROWT	Q83gl8 tropheryma	516	84	6.0	830	2	Q6C772_YARLI	Q6c772 yarrowia li
444	85	6.1	658	2	Q6XJH9_9ERIC	Q6xjh9 sideroxylon	517	84	6.0	935	2	Q9ZP04_TROMA	Q9zpo4 tropaeolum
445	85	6.1	658	2	Q6XJ14_9ERIC	Q6xj14 sideroxylon	518	84	6.0	4083	1	DYHC_ASHGO	Q9clm7 ashbya goss
446	85	6.1	821	2	Q2P9E8_XANOR	Q2p9e8 xanthomonas	519	83.5	6.0	261	1	Y1086_HAEIN	P45030 haemophilus
447	85	6.1	845	2	Q80Z08_MOUSE	Q80z08 mus musculu	520	83.5	6.0	295	2	Q9JVJ1_NEIMA	Q9jvj1 neisseria m
448	85	6.1	887	2	Q5H6R2_XANOR	Q5h6r2 xanthomonas	521	83.5	6.0	311	2	Q4R6X2_MACPA	Q4r6x2 macaca fasc
449	85	6.1	1166	1	ADCY6_RAT	Q03343 rattus norv	522	83.5	6.0	324	2	Q8XX91_RALSO	Q8xx91 ralstonia s
450	84.5	6.1	224	2	Q4T540_TETNG	Q4t540 tetraodon n	523	83.5	6.0	330	2	Q8AA46_BACTN	Q8aa46 bacteroides
451	84.5	6.1	269	2	Q837L9_ENTFA	Q837l9 enterococcu	524	83.5	6.0	333	2	Q8E4D6_STRAS	Q8e4d6 streptococc
452	84.5	6.1	283	2	Q65D18_BACLD	Q65d18 bacillus li	525	83.5	6.0	453	2	Q3MHV9_BOVIN	Q3mhv9 bos taurus
453	84.5	6.1	298	2	Q4COM7_CROWT	Q4com7 crocosphaer	526	83.5	6.0	468	2	Q8XKY8_CLOPE	Q8xky8 clostridium
454	84.5	6.1	323	2	Q7MYX3_PHOLL	Q7myx3 photorhabdu	527	83.5	6.0	480	2	Q5DYP6_VIBF1	Q5dyp6 vibrio fisc
455	84.5	6.1	333	2	Q3DMN2_STRAG	Q3dmn2 streptococc	528	83.5	6.0	481	2	Q4RQ81_TETNG	Q4rq81 tetraodon n
456	84.5	6.1	395	2	Q6ND83_RHOPA	Q6nd83 rhodopseudo	529	83.5	6.0	500	2	Q41JH6_METBU	Q41jh6 methanococc
457	84.5	6.1	401	2	Q2Y4J7_9ARCH	Q2y4j7 uncultured	530	83.5	6.0	509	2	Q8IA95_CAEBL	Q8ia95 caenorhabdi
458	84.5	6.1	405	2	Q65FD5_BACLD	Q65fd5 bacillus li	531	83.5	6.0	521	1	YJBC_SCHPO	Q74949 schizosacch
459	84.5	6.1	408	2	Q7XB13_WHEAT	Q7xb13 triticum ae	532	83.5	6.0	521	2	Q875S7_SACKL	Q875s7 saccharomyc
460	84.5	6.1	419	2	Q5P123_AZOSE	Q5p123 azoarcus sp	533	83.5	6.0	531	2	Q83EA0_COXBU	Q83ea0 coxiella bu
461	84.5	6.1	429	2	Q7Q0F3_ANOGA	Q7q0f3 anopheles g	534	83.5	6.0	605	2	Q9L1F6_STRCO	Q9l1f6 streptomyce
462	84.5	6.1	449	2	Q2TCQ8_9INSE	Q2tcq8 petrobis b	535	83.5	6.0	638	1	NU5M_PARLI	P12776 paracentrot
463	84.5	6.1	453	1	SERC1_HUMAN	Q9nrx5 homo sapien	536	83.5	6.0	693	2	Q85GD2_9DIPS	Q85gd2 nardostachy
464	84.5	6.1	453	2	Q9RNX3_RHIET	Q9rnrx3 rhizobium e	537	83.5	6.0	735	2	Q4WCR6_ASPFU	Q4wcr6 aspergillus
465	84.5	6.1	461	2	Q5ZMB5_CHICK	Q5zme5 gallus gall	538	83.5	6.0	736	2	Q9TJZ7_ANTHE	Q9tjz7 anthospermu
466	84.5	6.1	463	2	Q66C42_YERPS	Q66c42 yersinia ps	539	83.5	6.0	743	2	Q8WH76_9ASTE	Q8wh76 forgesia ra
467	84.5	6.1	463	2	Q8ZFW8_YERPE	Q8zfw8 yersinia pe	540	83.5	6.0	976	2	Q6FKX5_CANGA	Q6fkk5 candida gla
468	84.5	6.1	466	2	Q35PJ6_9BRAD	Q35pj6 bradyrhizob	541	83.5	6.0	1829	2	Q86HD9_DICDI	Q86hd9 dictyosteli
469	84.5	6.1	473	2	Q65N12_BACLD	Q65nl2 bacillus li	542	83.5	6.0	1867	2	Q551P7_DICDI	Q551p7 dictyosteli



543	83	6.0	234	2	Q3U8S2_MOUSE	Q3u8s2 mus musculus	616	82.5	5.9	669	2	Q3N287_9DELT	Q3n287 syntrophoba
544	83	6.0	241	1	YL068_MIMIV	Q5upe7 mimivirus.	617	82.5	5.9	671	2	Q751I3_ASHGO	Q751i3 ashbya goss
545	83	6.0	297	2	Q4KA95_PSEF5	Q4ka95 pseudomonas	618	82.5	5.9	680	2	Q8SL84_9DIPS	Q8sl84 valeriana j
546	83	6.0	305	2	Q8YWR6_ANASP	Q8ywr6 anabaena sp	619	82.5	5.9	680	2	Q70SP4_9LAMI	Q70sp4 limosella m
547	83	6.0	318	2	Q8DNJ4_STRR6	Q8dnj4 streptococc	620	82.5	5.9	704	2	Q9SCD0_9ERIC	Q9scd0 gustavia su
548	83	6.0	321	1	OR5V1_HUMAN	Q9ugf6 homo sapien	621	82.5	5.9	1121	2	Q4T7Y0_TETNG	Q4t7y0 tetraodon n
549	83	6.0	321	2	Q6NTB5_HUMAN	Q6ntb5 homo sapien	622	82.5	5.9	1363	2	Q7PPE3_ANOGA	Q7ppe3 anopheles g
550	83	6.0	321	2	Q5SQI9_HUMAN	Q5sqi9 homo sapien	623	82.5	5.9	1457	2	Q9HCE0_HUMAN	Q9hce0 homo sapien
551	83	6.0	324	2	Q4X186_ASPFU	Q4x186 aspergillus	624	82	5.9	219	2	Q75250_HUMAN	Q75250 homo sapien
552	83	6.0	361	2	Q3N8Q8_9PROT	Q3n8q8 nitrosomona	625	82	5.9	240	2	Q2ST72_MYCCA	Q2st72 mycoplasma
553	83	6.0	387	2	Q4AJC9_9CHLB	Q4ajc9 chlorobium	626	82	5.9	267	2	Q8HZ2_PSEPK	Q8hz2 pseudomonas
554	83	6.0	395	2	Q22QN4_SHEPU	Q2zqn4 shewanella	627	82	5.9	299	1	T2R16_RAT	Q9jku0 rattus norv
555	83	6.0	395	2	Q36F10_9GAMM	Q36fi0 shewanella	628	82	5.9	313	2	Q87GV0_VIBPA	Q87gv0 vibrio para
556	83	6.0	397	2	Q41BF8_9BACI	Q41bf8 exiguobacte	629	82	5.9	317	2	Q9K6Y6_BACHD	Q9k6y6 bacillus ha
557	83	6.0	427	2	Q7P8Q1_RICSI	Q7p8q1 rickettsia	630	82	5.9	327	2	Q9KT03_VIBCH	Q9kt03 vibrio chol
558	83	6.0	427	2	Q92HP5_RICCN	Q92hp5 rickettsia	631	82	5.9	339	2	Q84ET2_9PROC	Q84et2 uncultured
559	83	6.0	457	2	Q8ULB5_PYRFU	Q8ule5 pyrococcus	632	82	5.9	347	2	Q4IU66_AZОВI	Q4iu66 azotobacter
560	83	6.0	460	2	Q9V0Y7_PYRAB	Q9v0y7 pyrococcus	633	82	5.9	356	2	Q9FZ96_ARATH	Q9fz96 arabidopsis
561	83	6.0	466	2	Q7VNG8_HAEDU	Q7vng8 haemophilus	634	82	5.9	356	2	Q9M7R1_ARATH	Q9m7r1 arabidopsis
562	83	6.0	467	2	Q6P9F8_ACIAD	Q6f9f8 acinetobact	635	82	5.9	359	2	Q97C50_THEVO	Q97c50 thermoplasm
563	83	6.0	474	2	Q3GPF2_9GAMM	Q3gpf2 psychrobact	636	82	5.9	365	2	Q5M7L7_XENTR	Q5m7l7 xenopus tro
564	83	6.0	496	2	Q9I4I8_PSEAB	Q9i4i8 pseudomonas	637	82	5.9	389	2	Q25590_HELPE	Q25590 helicobacte
565	83	6.0	508	2	Q2TY23_ASPOR	Q2ty23 aspergillus	638	82	5.9	392	2	Q40GS4_9RHOB	Q40gs4 jannaschia
566	83	6.0	511	2	Q5V404_HALMA	Q5v404 haloarcula	639	82	5.9	395	2	Q35ZL1_9GAMM	Q35zl1 shewanella
567	83	6.0	554	2	Q2Y8N1_NITMU	Q2y8n1 nitrosospir	640	82	5.9	395	2	Q3Q6Y1_9GAMM	Q3q6y1 shewanella
568	83	6.0	587	2	Q87TZ8_PSESM	Q87tz8 pseudomonas	641	82	5.9	405	2	Q983X3_RHILO	Q983x3 rhizobium l
569	83	6.0	637	1	NU5M_STRPU	P15552 strongyloce	642	82	5.9	412	2	Q5IA38_AMBTC	Q5ia38 amborella t
570	83	6.0	787	2	Q3J591_RHOS4	Q3j591 rhodobacter	643	82	5.9	415	2	Q3KSU4_PSEPF	Q3ksu4 pseudomonas
571	83	6.0	802	2	Q8SZ78_DROME	Q8sz78 drosophila	644	82	5.9	441	2	Q3VTV3_PROAB	Q3vtv3 prosthecocch
572	83	6.0	1139	2	Q66DQ6_YERPS	Q66dq6 yersinia ps	645	82	5.9	446	1	CITN_KLEPN	P31602 klebsiella
573	83	6.0	1635	2	Q9CLI7_MYCGR	Q9cli7 mycosphaere	646	82	5.9	459	2	Q70XF0_DROAU	Q70xf0 dromiciops
574	83	6.0	2159	2	Q8RUQ1_MAIZE	Q8ruq1 zea mays (m	647	82	5.9	465	2	Q74M77_NANEQ	Q74m77 nanoarchaeu
575	83	6.0	2159	2	Q8RVL1_MAIZE	Q8rvl1 zea mays (m	648	82	5.9	485	2	Q3RUF1_RALME	Q3ruf1 ralstonia m
576	82.5	5.9	265	2	Q3P3G5_9GAMM	Q3p3g5 shewanella	649	82	5.9	488	2	Q93YP9_ARATH	Q93yp9 arabidopsis
577	82.5	5.9	271	2	Q3ORV7_THIDN	Q3orv7 thiomicrosp	650	82	5.9	494	2	Q6F0R2_MESFL	Q6f0r2 mesoplasma
578	82.5	5.9	281	2	Q83BV7_COXBU	Q83bv7 coxiella bu	651	82	5.9	497	2	Q97A43_THEVO	Q97a43 thermoplasm
579	82.5	5.9	337	2	Q59QT6_CANAL	Q59qt6 candida alb	652	82	5.9	497	2	Q421K2_DESHA	Q42lk2 desulfitoba
580	82.5	5.9	346	2	Q8TQ84_METAC	Q8tc84 methanosarc	653	82	5.9	498	2	Q73GW3_WOLPM	Q73gw3 wolbachia p
581	82.5	5.9	361	2	Q31I62_THICR	Q31i62 thiomicrosp	654	82	5.9	514	2	Q44WQ6_9BURK	Q44wq6 burkholderi
582	82.5	5.9	368	2	Q72KY8_THET2	Q72ky8 thermus the	655	82	5.9	514	2	Q4LNM2_2BURK	Q4lnm2 burkholderi
583	82.5	5.9	391	1	EPT1_YEAST	P22i40 saccharomyc	656	82	5.9	528	2	Q40LE0_DESAC	Q40le0 desulfuromo
584	82.5	5.9	400	2	Q7M9I6_WOLSU	Q7m9i6 wolinnella s	657	82	5.9	545	2	Q8FNV5_COREF	Q8fnv5 corynebacte
585	82.5	5.9	402	2	Q4HY9_GIBZE	Q4hy9 gibberella	658	82	5.9	548	2	Q9A8F3_CAUCR	Q9a8f3 caulobacter
586	82.5	5.9	418	2	Q9HXM9_PSEAE	Q9hxm9 pseudomonas	659	82	5.9	557	1	YQ4_SCHPO	Q74537 schizosacch
587	82.5	5.9	432	2	Q35G00_9BRAD	Q35g00 bradyrhizob	660	82	5.9	557	2	Q8G3S6_BIFLO	Q8g3s6 bifidobacte
588	82.5	5.9	432	2	Q5PE07_SALPA	Q5pe07 salmonella	661	82	5.9	573	2	Q09932_CABEL	Q09932 caenorhabdi
589	82.5	5.9	437	2	Q8IKE3_PLAF7	Q8ike3 plasmodium	662	82	5.9	594	2	Q7T709_9CLOS	Q7t709 citrus tris
590	82.5	5.9	439	2	Q4UYJ1_XANC8	Q4uyj1 xanthomonas	663	82	5.9	604	2	Q32UR9_SMICR	Q32ur9 sminthopsis
591	82.5	5.9	439	2	Q8P5I4_XANCP	Q8p5i4 xanthomonas	664	82	5.9	673	2	Q2RGF9_MOOTH	Q2rgf9 moorella th
592	82.5	5.9	441	2	Q3BPG6_XANC5	Q3bp66 xanthomonas	665	82	5.9	706	2	Q45283_CAEEL	Q45283 caenorhabdi
593	82.5	5.9	443	2	Q2P6S4_XANOR	Q2p6s4 xanthomonas	666	82	5.9	727	2	Q5A438_CANAL	Q5a438 candida alb
594	82.5	5.9	448	2	Q6DVM4_9CRUS	Q6dvm4 triops long	667	82	5.9	748	2	Q6A6C2_PROAC	Q6a6c2 propionibac
595	82.5	5.9	451	2	Q82CI8_STRAW	Q82ci8 streptomyce	668	82	5.9	766	2	Q3PHL5_PARDE	Q3phl5 paracoccus
596	82.5	5.9	452	2	Q9ZKR4_HELPTJ	Q9zkr4 helicobacte	669	82	5.9	786	2	Q385S3_9TRYP	Q385s3 trypanosoma
597	82.5	5.9	453	2	Q5RCN8_PONPY	Q5rcn8 pongo pygma	670	82	5.9	807	2	Q3BYI7_XANC5	Q3byi7 xanthomonas
598	82.5	5.9	456	2	Q3K677_PSEPF	Q3k677 pseudomonas	671	82	5.9	881	2	Q6F8D1_ACIAD	Q6f8d1 acinetobact
599	82.5	5.9	462	2	Q6F0L1_MESFL	Q6f0l1 mesoplasma	672	82	5.9	884	2	Q8ER30_OCEIH	Q8er30 oceanobacil
600	82.5	5.9	471	2	Q8SS9_LACPL	Q8ss9 lactobacill	673	82	5.9	893	2	Q511Z0_ENTHI	Q511z0 entamoeba h
601	82.5	5.9	478	2	Q368A8_9GAMM	Q368a8 shewanella	674	82	5.9	1029	2	Q6KAN9_MOUSE	Q6kan9 mus musculu
602	82.5	5.9	478	2	Q2Z3J4_9GAMM	Q2z3j4 shewanella	675	82	5.9	1117	2	Q2UGL8_ASPOR	Q2ugl8 aspergillus
603	82.5	5.9	478	2	Q8EEL5_SHEON	Q8eel5 shewanella	676	82	5.9	1139	2	Q8ZC91_YERPE	Q8zc91 yersinia pe
604	82.5	5.9	482	2	Q3JD04_NITOC	Q3jd04 nitrosococc	677	82	5.9	1156	2	Q74WP6_YERPE	Q74wp6 yersinia pe
605	82.5	5.9	484	2	Q44H18_CHRSL	Q44h18 chromohalob	678	82	5.9	1168	1	ADCY6_HUMAN	Q43306 homo sapien
606	82.5	5.9	486	2	Q82YJ7_ENTFA	Q82yj7 enterococcu	679	82	5.9	1611	2	Q2U3YI_ASPOR	Q2u3yl aspergillus
607	82.5	5.9	494	1	NU4M_TRIRU	Q36834 trichophyto	680	81.5	5.9	205	2	Q8CYE9_STRR6	Q8cye9 streptococc
608	82.5	5.9	508	2	Q950R5_SPIPN	Q950r5 spizellomyc	681	81.5	5.9	205	2	Q97PC0_STRPN	Q97pc0 streptococc
609	82.5	5.9	543	2	Q7Z5I7_HUMAN	Q7z5i7 homo sapien	682	81.5	5.9	257	2	Q39XJ4_GEOMG	Q39xj4 geobacter m
610	82.5	5.9	548	2	Q6AAJ7_PROAC	Q6aaJ7 propionibac	683	81.5	5.9	268	2	Q7MKQ7_VIBVY	Q7mkq7 vibrio vuln
611	82.5	5.9	596	1	AGP2_YEAST	P38090 saccharomyc	684	81.5	5.9	268	2	Q8D9M9_VIBVU	Q8d9m9 vibrio vuln
612	82.5	5.9	620	2	Q7SSR8_NEUCR	Q7ssr8 neurospora	685	81.5	5.9	292	2	Q4JT26_CORJK	Q4jt26 corynebacte
613	82.5	5.9	623	2	Q98P35_RHILO	Q98p35 rhizobium l	686	81.5	5.9	292	2	Q92DG0_LISIN	Q92dg0 listeria in
614	82.5	5.9	636	2	Q5KSS3_9ECHI	Q5kss3 ludidia quin	687	81.5	5.9	307	1	UPPP2_CLOAB	Q97kf6 clostridium
615	82.5	5.9	640	2	Q6MB47_PARUW	Q6mb47 parachlamyd	688	81.5	5.9	321	2	Q94VH0_VARGO	Q94vh0 varanus gou



689	81.5	5.9	325	2	Q973Q6_SULTO	Q973q6	sulfolobus	762	81	5.8	411	2	Q2LS96_9DELT	Q2ls96	syntrophus
690	81.5	5.9	351	2	Q9FZ95_ARATH	Q9fz95	arabidopsis	763	81	5.8	422	2	Q6ESP5_ORYSA	Q6esp5	oryza sativ
691	81.5	5.9	390	2	Q5BDJ8_EMENI	Q5bdj8	aspergillus	764	81	5.8	422	2	Q8Y1K4_FALSO	Q8y1k4	ralstonia s
692	81.5	5.9	399	2	Q8NCC4_HUMAN	Q8ncc4	homo sapien	765	81	5.8	423	2	Q3ZXW4_DEHSC	Q3zxw4	dehalococco
693	81.5	5.9	410	2	Q5NGS9_FRATT	Q5ngs9	francisella	766	81	5.8	438	2	Q8X4U5_ECO57	Q8x4u5	escherichia
694	81.5	5.9	422	2	Q3VVI4_PROAE	Q3vvi4	prosthecoch	767	81	5.8	446	2	Q3GMW8_9GAMM	Q3gmw8	psychrobact
695	81.5	5.9	423	2	Q2Z9R5_9GAMM	Q2z9r5	shewanella	768	81	5.8	461	1	PUUP_ECOLI	P76037	escherichia
696	81.5	5.9	423	2	Q360D7_9GAMM	Q360d7	shewanella	769	81	5.8	461	2	Q31Z22_SHIBS	P76037	escherichia
697	81.5	5.9	423	2	Q36EP5_9GAMM	Q36ep5	shewanella	770	81	5.8	471	2	Q4S3Y1_TETNG	Q4s3y1	tetraodon n
698	81.5	5.9	425	2	Q88CV8_PSEPK	Q88cv8	pseudomonas	771	81	5.8	479	2	Q87155_VIBCH	Q87155	vibrio chol
699	81.5	5.9	435	2	Q4YAK0_PLABE	Q4yak0	plasmodium	772	81	5.8	479	2	Q5H778_ECOLI	Q5h778	escherichia
700	81.5	5.9	436	2	Q7YZ03_CRYPV	Q7yz03	cryptospori	773	81	5.8	483	2	Q624N5_CAEBR	Q624n5	caenorhabdi
701	81.5	5.9	438	2	Q9HUD9_PSEAE	Q9hud9	pseudomonas	774	81	5.8	485	2	Q7PQT4_ANOGA	Q7pqt4	anopheles g
702	81.5	5.9	446	2	Q60WD5_CAEBR	Q60wd5	caenorhabdi	775	81	5.8	487	2	Q9FRL3_ARATH	Q9frl3	arabidopsis
703	81.5	5.9	454	2	Q48KP6_PSEI14	Q48kp6	pseudomonas	776	81	5.8	515	2	Q8TF71_HUMAN	Q8tf71	homo sapien
704	81.5	5.9	454	2	Q4ZVE0_PSEU2	Q4zve0	pseudomonas	777	81	5.8	531	2	Q3KCC6_PSEPF	Q3kcc6	pseudomonas
705	81.5	5.9	454	2	Q884R2_PSESM	Q884r2	pseudomonas	778	81	5.8	544	1	YRT3_CAEEL	Q10046	caenorhabdi
706	81.5	5.9	454	2	Q89WU1_BRAJA	Q89wu1	bradyrhizob	779	81	5.8	548	2	Q8AA29_BACTN	Q8aa29	bacteroides
707	81.5	5.9	463	2	Q5DBJ2_SCHJA	Q5dbj2	schistosoma	780	81	5.8	550	2	Q7NZQ0_CHRVO	Q7nzzq0	chromobacte
708	81.5	5.9	466	2	Q2QI38_9NEOP	Q2qi38	adoxophyes	781	81	5.8	578	2	Q47F72_DECAR	Q47f72	dechloromon
709	81.5	5.9	467	2	Q9W1Z2_DROME	Q9wlz2	drosophila	782	81	5.8	595	2	Q91MJ8_9PARA	Q91mj8	menangle vi
710	81.5	5.9	475	2	Q33RV8_9GAMM	Q33rv8	shewanella	783	81	5.8	603	2	Q3N807_9PROT	Q3n807	nitrosomona
711	81.5	5.9	482	2	Q3JEF5_NITOC	Q3jef5	nitrosococc	784	81	5.8	608	2	Q7QP79_GIALA	Q7qp79	giardia lam
712	81.5	5.9	485	2	Q18063_CAEEL	Q18063	caenorhabdi	785	81	5.8	647	2	Q9GEU0_SAMVA	Q9geu0	samolus val
713	81.5	5.9	485	2	Q8SYB7_DROME	Q8syb7	drosophila	786	81	5.8	657	2	Q6XJ11_9ERIC	Q6xj11	sideroxylon
714	81.5	5.9	485	2	Q9W1Z3_DROME	Q9wlz3	drosophila	787	81	5.8	686	2	Q47L56_THEFY	Q47l56	thermobifid
715	81.5	5.9	487	2	Q2NA79_9SPHN	Q2na79	erythroba	788	81	5.8	724	2	Q9GF06_9ERIC	Q9gf06	bonellia um
716	81.5	5.9	510	2	Q34523_FASHE	Q34523	fasciola he	789	81	5.8	734	2	Q9THV8_9GENT	Q9thv8	rondeletia
717	81.5	5.9	513	2	Q31ET8_THICR	Q3iet8	thiomicrosp	790	81	5.8	743	2	Q61LV8_CAEBR	Q61lv8	caenorhabdi
718	81.5	5.9	517	2	Q4HUN6_GIBZE	Q4hun6	gibberella	791	81	5.8	829	2	Q3N9X2_9PROT	Q3n9x2	nitrosomona
719	81.5	5.9	524	2	Q4SNU4_TETNG	Q4snu4	tetraodon n	792	81	5.8	865	2	Q2Y411_9ARCH	Q2y411	uncultured
720	81.5	5.9	527	2	Q2NHK7_9EURY	Q2nhk7	methanospa	793	81	5.8	875	2	Q9V8U1_DROME	Q9v8u1	drosophila
721	81.5	5.9	535	2	Q3J012_RHOS4	Q3j012	rhodobacter	794	81	5.8	889	2	Q4V5E4_DROME	Q4v5e4	drosophila
722	81.5	5.9	535	2	Q53111_RHOSH	Q53111	rhodobacter	795	81	5.8	971	2	Q68XX4_RICTY	Q68xx4	rickettsia
723	81.5	5.9	570	2	Q2SVK8_BURTH	Q2svk8	burkholderi	796	81	5.8	1102	2	Q88CW3_PSEPK	Q88cw3	pseudomonas
724	81.5	5.9	577	2	Q2U0M4_ASPOR	Q2u0m4	aspergillus	797	81	5.8	1150	2	Q2XJ80_PSEPU	Q2xj80	pseudomonas
725	81.5	5.9	615	2	Q2U0X1_ASPOR	Q2u0x1	aspergillus	798	81	5.8	1207	2	Q4P6A9_USTMA	Q4p6a9	ustilago ma
726	81.5	5.9	618	2	Q5AY73_EMENI	Q5ay73	aspergillus	799	81	5.8	2186	1	POLG_CXB20	Q9ylg5	c genome po
727	81.5	5.9	623	2	Q519X5_ENTHI	Q519x5	entamoeba h	800	81	5.8	162	2	Q7NN16_GLOVI	Q7nn16	gloeobacter
728	81.5	5.9	626	2	Q8XUM7_RALSO	Q8xum7	ralstonia s	801	80.5	5.8	256	2	Q30UH8_THIDN	Q30uh8	thiomicrosp
729	81.5	5.9	711	2	Q6LH73_PROPR	Q6lh73	photobacter	802	80.5	5.8	261	2	Q6LTB2_PHOPR	Q6ltb2	photobacter
730	81.5	5.9	713	2	Q9VWG4_DROME	Q9vwg4	drosophila	803	80.5	5.8	288	2	Q85JA0_CLOSI	Q85ja0	clonorchis
731	81.5	5.9	724	2	Q8MRA8_DROME	Q8mra8	drosophila	804	80.5	5.8	291	2	Q746X4_GEOSL	Q746x4	geobacter s
732	81.5	5.9	724	2	Q9TJZ6_9GENT	Q9tjz6	alseis lugo	805	80.5	5.8	296	2	Q3EEG9_ACTSC	Q3ee9	actinobacil
733	81.5	5.9	731	2	Q9TJT2_9GENT	Q9tjt2	hillia trif	806	80.5	5.8	316	2	Q2VYV6_MAGSA	Q2vyv6	magnetospir
734	81.5	5.9	732	2	Q9TJS0_9GENT	Q9tjs0	pogonopus s	807	80.5	5.8	321	2	Q647F8_9VIRU	Q647f8	thermoprote
735	81.5	5.9	734	2	Q98706_9GENT	Q98706	chiococca r	808	80.5	5.8	324	2	Q94VD4_9SAUR	Q94vd4	varanus pan
736	81.5	5.9	741	2	Q71QV9_9ASTR	Q71qv9	sigesbeckia	809	80.5	5.8	333	2	Q83ZZ6_9GAMM	Q83zz6	lamprocysti
737	81.5	5.9	745	2	Q5UYP6_HALMA	Q5uyvp6	haloarcula	810	80.5	5.8	333	2	Q81HX6_PLAF7	Q8ihx6	plasmodium
738	81.5	5.9	855	2	Q6BGA9_PARTE	Q6bga9	paramecium	811	80.5	5.8	334	2	Q6AWL9_DROME	Q6awl9	drosophila
739	81.5	5.9	893	2	Q54BC6_DICDI	Q54bc6	dictyosteli	812	80.5	5.8	334	2	Q81QJ7_DROME	Q8iqj7	drosophila
740	81.5	5.9	1402	2	Q610A1_CAEBR	Q610a1	caenorhabdi	813	80.5	5.8	354	1	PCBG_PROMT	Q46jw4	prochloroco
741	81	5.8	226	2	Q4MVG5_BACCE	Q4mvg5	bacillus ce	814	80.5	5.8	359	2	Q5HD36_STAAC	Q5hd36	staphylococ
742	81	5.8	226	2	Q816R9_BACCR	Q816r9	bacillus ce	815	80.5	5.8	359	2	Q6G6F7_STAAS	Q6g6f7	staphylococ
743	81	5.8	228	2	Q4L948_STAHI	Q4l948	staphylococ	816	80.5	5.8	359	2	Q79ZZ9_STAAM	Q79zz9	staphylococ
744	81	5.8	273	2	Q3GLF0_9GAMM	Q3glf0	psychrobact	817	80.5	5.8	359	2	Q7A3I4_STAAN	Q7a3i4	staphylococ
745	81	5.8	287	2	Q5V2C4_HALMA	Q5v2c4	haloarcula	818	80.5	5.8	359	2	Q99RB8_STAAM	Q99rb8	staphylococ
746	81	5.8	293	1	Y417_CHLTR	O84422	chlamydia t	819	80.5	5.8	360	2	Q7Q2N8_ANOGA	Q7q2n8	anopheles g
747	81	5.8	293	2	Q92WD8_RHIME	Q92wd8	rhizobium m	820	80.5	5.8	366	2	Q8CWZ5_STRMU	Q8cwz5	streptococc
748	81	5.8	296	2	Q3SMM5_THIDA	Q3smm5	thiobacillu	821	80.5	5.8	368	2	Q610H8_CAEBR	Q610h8	caenorhabdi
749	81	5.8	297	2	Q5NMK8_ZYMMO	Q5nmk8	zymomonas m	822	80.5	5.8	368	2	Q47GR9_DECAR	Q47gr9	dechloromon
750	81	5.8	305	2	Q3M361_ANAVT	Q3m361	anabaena va	823	80.5	5.8	373	2	Q5YN20_NOCPA	Q5yn20	nocardia fa
751	81	5.8	305	2	Q5J3L3_RAT	Q5j3l3	rattus norv	824	80.5	5.8	393	2	Q5HM49_STAEO	Q5hm49	staphylococ
752	81	5.8	313	1	REN_VIEVU	Q8dds2	vibrio vuln	825	80.5	5.8	393	2	Q8CNG2_STAES	Q8cng2	staphylococ
753	81	5.8	313	1	RBN_VIBVY	Q7mq07	vibrio vuln	826	80.5	5.8	419	2	Q81NE5_BACAN	Q81ne5	bacillus an
754	81	5.8	315	2	Q3HAB6_TRIER	Q3hab6	trichodesmi	827	80.5	5.8	433	2	Q74XD2_YERPE	Q74xd2	yersinia pe
755	81	5.8	347	2	Q2WPS2_CLOBE	Q2wps2	clostridium	828	80.5	5.8	433	2	Q66FD9_YERPS	Q66fd9	yersinia ps
756	81	5.8	369	2	Q3BU19_XANC5	Q3bu19	xanthomonas	829	80.5	5.8	433	2	Q8Z1Y7_YERPE	Q8ziy7	yersinia pe
757	81	5.8	375	1	PCBC_PROHO	P95505	prochloroth	830	80.5	5.8	438	2	Q87VV4_PSESM	Q87vv4	pseudomonas
758	81	5.8	375	2	Q5NED7_ZYMMO	Q5npd7	zymomonas m	831	80.5	5.8	446	2	Q951C1_TETTH	Q951c1	tetrahymena
759	81	5.8	382	2	Q9IBP4_CYPCA	Q9ibp4	cyprinus ca	832	80.5	5.8	453	2	Q618Q8_CAEBR	Q618q8	caenorhabdi
760	81	5.8	396	2	Q83KE0_SHIFL	Q83ke0	shigella fl	833	80.5	5.8	454	2	Q4K8P3_PSEF5	Q4k8p3	pseudomonas
761	81	5.8	411	2	Q3NRE2_SHEFR	Q3nre2	shewanella	834	80.5	5.8					

835	80.5	5.8	465	2	Q48D16_PSE14	Q48d16 pseudomonas	908	80	5.7	451	2	Q617X8_LEPDU	Q6i7x8 leptotyphlo
836	80.5	5.8	469	2	P93561_SOLTU	P93561 solanum tub	909	80	5.7	463	2	Q2Y9L3_NITMU	Q2y9l3 nitrosospir
837	80.5	5.8	470	2	Q9CP91_PASMU	Q9cp91 pasteurella	910	80	5.7	472	2	Q9N5Q8_CAEEL	Q9n5q8 caenorhabdi
838	80.5	5.8	472	2	Q44YB5_9BURK	Q44yb5 burkholderi	911	80	5.7	488	2	Q55GU7_DICDI	Q55gu7 dictyosteli
839	80.5	5.8	472	2	Q44YSU9_9BURK	Q44ysu9 burkholderi	912	80	5.7	488	2	Q966D7_CABEL	Q966d7 caenorhabdi
840	80.5	5.8	473	1	IOLT_BACSU	Q34718 bacillus su	913	80	5.7	512	2	Q4WFT2_ASPFU	Q4wft2 aspergillus
841	80.5	5.8	475	2	Q6LR41_PHOPR	Q6lr41 photobacter	914	80	5.7	516	2	Q94JG1_ORYSA	Q94jg1 oryza sativ
842	80.5	5.8	478	2	Q3QDD4_9GAMM	Q3qdd4 shewanella	915	80	5.7	528	2	Q50ZV7_ENTHI	Q50zv7 entamoeba h
843	80.5	5.8	518	2	Q2SG80_9GAMM	Q2sg80 shabella che	916	80	5.7	558	2	Q6XRA4_9BACT	Q6xra4 uncultured
844	80.5	5.8	523	2	Q8AAX1_BACTN	Q8aax1 bacteroides	917	80	5.7	657	2	Q6XJM6_9ERIC	Q6xjm6 inhambanell
845	80.5	5.8	528	2	Q5F6U6_NEIG1	Q5f6u6 neisseria g	918	80	5.7	671	2	Q7WXB7_RALEU	Q7wxb7 ralstonia e
846	80.5	5.8	528	2	Q7DDN3_NEIMB	Q7ddn3 neisseria m	919	80	5.7	686	2	Q3HT50_9BORA	Q3ht50 coldenia pr
847	80.5	5.8	528	2	Q9JRD7_NEIMA	Q9jrd7 neisseria m	920	80	5.7	699	2	Q9TLF3_9LAMI	Q9tlf3 hemiphragma
848	80.5	5.8	531	2	Q6KI84_MYCMO	Q6ki84 mycoplasma	921	80	5.7	702	2	Q19823_9LAMI	Q19823 alsobia sp.
849	80.5	5.8	534	2	Q2U2A8_ASPOR	Q2u2a8 aspergillus	922	80	5.7	714	2	Q73Y59_MYCPA	Q73y59 mycobacteri
850	80.5	5.8	536	2	Q6MEN5_PARUW	Q6men5 parachlamyd	923	80	5.7	740	2	Q9TJU4_CEOC	Q9tju4 cephalanthu
851	80.5	5.8	583	2	Q4ELG7_LISMO	Q4elg7 listeria mo	924	80	5.7	740	2	Q5PG25_SALTY	Q5pg25 salmonella
852	80.5	5.8	590	1	CAN1_YEAST	P04817 saccharomyc	925	80	5.7	740	2	Q8ZQN3_SALTY	Q8zqn3 salmonella
853	80.5	5.8	595	2	Q3J3B7_RHOS4	Q3j3b7 rhodobacter	926	80	5.7	850	2	Q3M4P3_ANAVT	Q3m4p3 anabaena va
854	80.5	5.8	637	2	Q21277_RECAM	O21277 reclinomona	927	80	5.7	862	2	Q3VGR9_9SPHN	Q3vgr9 sphingopyxi
855	80.5	5.8	660	2	Q891N8_CLOTE	Q891n8 clostridium	928	80	5.7	902	2	Q9K9X9_BACHD	Q9k9x9 bacillus ha
856	80.5	5.8	671	2	Q34G29_RHOPA	Q34g29 rhodopsium	929	80	5.7	1067	2	Q8EJ80_SHEON	Q8ej80 shewanella
857	80.5	5.8	690	2	Q2IM16_9DELT	Q2im16 anaeromyxob	930	80	5.7	1123	2	Q9LYR7_ARATH	Q9lyr7 arabidopsis
858	80.5	5.8	728	2	Q98702_9GENT	O98702 luculia gra	931	80	5.7	1202	2	Q4WP24_ASPFU	Q4wp24 aspergillus
859	80.5	5.8	732	2	Q9TJY9_CALCA	Q9tjy9 calycophyll	932	80	5.7	1480	2	Q6C5L2_YARLI	Q6c5l2 yarrowia li
860	80.5	5.8	751	2	Q3S0G1_RALME	Q3s0g1 ralstonia m	933	79.5	5.7	225	2	Q347J9_RHOPA	Q347j9 rhodopseudo
861	80.5	5.8	812	2	Q55KN8_CRYNE	Q55kn8 cryptococcu	934	79.5	5.7	234	2	Q6JCS9_9HEMI	Q6jcs9 aleuroplatu
862	80.5	5.8	812	2	Q5KAT6_CRYNE	Q5kat6 cryptococcu	935	79.5	5.7	235	2	Q57RE9_SALCH	Q57re9 salmonella
863	80.5	5.8	834	1	SL9A3_HUMAN	P48764 homo sapien	936	79.5	5.7	254	2	Q2ZGU0_CALSA	Q2zgu0 caldicellul
864	80.5	5.8	834	2	Q3MIW3_HUMAN	Q3miw3 homo sapien	937	79.5	5.7	260	2	Q3EIP1_ACTSC	Q3eip1 actinobacil
865	80.5	5.8	1019	2	Q3HAM2_TRIER	Q3ham2 trichodesmi	938	79.5	5.7	261	2	Q31GZ8_THICR	Q31gz8 thiomicrosp
866	80	5.7	210	2	Q5VWM7_HUMAN	Q5vwm7 homo sapien	939	79.5	5.7	264	2	Q6ITH2_CERBA	Q6ith2 cercaria ba
867	80	5.7	226	2	Q81KJ3_BACAN	Q81kj3 bacillus an	940	79.5	5.7	264	2	Q6ITI1_CERBA	Q6iti1 cercaria ba
868	80	5.7	266	2	Q9HXP7_PSEAE	Q9hxp7 pseudomonas	941	79.5	5.7	293	2	Q3PJM4_PARDE	Q3pjm4 paracoccus
869	80	5.7	268	2	Q76FP9_STYPL	Q76fp9 styela plic	942	79.5	5.7	293	2	Q66D49_YERPS	Q66d49 yersinia ps
870	80	5.7	270	2	Q5JE18_PYRKO	Q5je18 pyrococcus	943	79.5	5.7	296	2	Q93KC0_ERWCH	Q93kc0 erwinia chr
871	80	5.7	273	2	Q4AWQ6_9BURK	Q4awq6 polaromonas	944	79.5	5.7	296	2	Q6D4I7_ERWCT	Q6d4i7 erwinia car
872	80	5.7	277	2	Q3EQN3_BACTI	Q3eqn3 bacillus th	945	79.5	5.7	297	2	Q7U561_SVNPX	Q7u561 synechococc
873	80	5.7	277	2	Q818H6_BACCR	Q818h6 bacillus ce	946	79.5	5.7	298	2	Q8R257_MOUSE	Q8r257 mus musculu
874	80	5.7	285	2	Q6YQJ4_ONYPE	Q6yqj4 onion yello	947	79.5	5.7	308	2	Q6CTH9_KLJULA	Q6cth9 kluyveromyc
875	80	5.7	286	2	Q4MMH9_BACCE	Q4mmh9 bacillus ce	948	79.5	5.7	308	2	Q6ACY4_LEIXX	Q6acy4 leifsonia x
876	80	5.7	286	2	Q63CM0_BACCZ	Q63cm0 bacillus ce	949	79.5	5.7	312	2	Q5AF82_CANAL	Q5af82 candida alb
877	80	5.7	286	2	Q6HK25_BACHK	Q6hk25 bacillus th	950	79.5	5.7	317	2	Q7UKZ3_RHOBA	Q7ukz3 rhodopirell
878	80	5.7	286	2	Q81RV2_BACAN	Q81rv2 bacillus an	951	79.5	5.7	323	2	Q8DUD9_STRMU	Q8dud9 streptococc
879	80	5.7	289	2	Q5DVU0_MIMPU	Q5dvu0 mimosa pud	952	79.5	5.7	325	2	Q4NG89_9MICC	Q4ng89 arthrobacte
880	80	5.7	291	2	Q8UIQ9_AGR5T	Q8uiq9 agrobacteri	953	79.5	5.7	329	2	Q4SJT4_TETNG	Q4sjt4 tetraodon n
881	80	5.7	293	2	Q3KLT6_CHLTA	Q3klt6 chlamydia t	954	79.5	5.7	342	2	Q5KY68_GEOKA	Q5ky68 geobacillus
882	80	5.7	296	2	Q4MPJ0_BACCE	Q4mpj0 bacillus ce	955	79.5	5.7	370	2	Q35QS4_9BRAD	Q35qs4 bradyrhizob
883	80	5.7	299	2	Q6AL50_DESPS	Q6al50 desulfotale	956	79.5	5.7	371	2	Q2USP9_ASPOR	Q2usp9 aspergillus
884	80	5.7	301	2	Q2RGF6_MOOTH	Q2rgf6 moorella th	957	79.5	5.7	384	2	Q88ZD3_LACPL	Q88zd3 lactobacili
885	80	5.7	306	2	Q2K6L6_RHIET	Q2k6l6 rhizobium e	958	79.5	5.7	386	2	Q2KA16_RHIET	Q2ka16 rhizobium e
886	80	5.7	312	2	Q44JP5_CHRSL	Q44jp5 chromohalob	959	79.5	5.7	388	2	Q40EB4_9RHOB	Q40eb4 jannaschia
887	80	5.7	322	2	Q9GEH0_9MYRT	Q9geh0 memecylon b	960	79.5	5.7	398	2	Q7NVC7_CHRVO	Q7nvc7 chromobacte
888	80	5.7	339	2	Q84ET1_9PROC	Q84et1 prochloroth	961	79.5	5.7	405	2	Q77085_CABEL	Q77085 caenorhabdi
889	80	5.7	341	2	Q47IB7_DECAR	Q47ib7 dechloromon	962	79.5	5.7	434	2	Q5E758_VIBF1	Q5e758 vibrio fisc
890	80	5.7	357	2	Q3PQV7_NITHA	Q3pqv7 nitrobacter	963	79.5	5.7	443	2	Q95AK6_9ASTR	Q95ak6 dialypetalu
891	80	5.7	363	2	Q8KR39_CLOSG	Q8kr39 clostridium	964	79.5	5.7	445	2	Q5S937_SYNY3	Q5s937 synechocyst
892	80	5.7	364	2	Q2Y635_NITMU	Q2y635 nitrosospir	965	79.5	5.7	445	2	Q6HKB2_BACHK	Q6hkb2 bacillus th
893	80	5.7	364	2	Q51723_BACNO	Q51723 bacteroides	966	79.5	5.7	453	2	Q2JYF1_RHIET	Q2jyf1 rhizobium e
894	80	5.7	370	2	Q4DUS8_TRYCR	Q4dus8 trypanosoma	967	79.5	5.7	454	2	Q3K8Y3_PSEFF	Q3k8y3 pseudomonas
895	80	5.7	380	2	Q4RMW9_TETNG	Q4rmw9 tetraodon n	968	79.5	5.7	461	2	Q83RL6_SHIFL	Q83rl6 shigella fl
896	80	5.7	381	2	Q3IIN3_PSEHT	Q3iin3 pseudoalter	969	79.5	5.7	466	2	Q4WS19_ASPFU	Q4ws19 aspergillus
897	80	5.7	386	2	Q4MM07_BACCE	Q4mm07 bacillus ce	970	79.5	5.7	466	2	Q4KYL0_CAPBU	Q4kylo capsella bu
898	80	5.7	387	2	Q55IJ1_CRYNE	Q55ij1 cryptococcu	971	79.5	5.7	479	2	Q3Z144_SHISS	Q3z144 shigella so
899	80	5.7	390	2	Q3NLQ4_SHEFR	Q3nlq4 shewanella	972	79.5	5.7	483	2	Q31J91_THICR	Q31j91 thiomicrosp
900	80	5.7	391	2	Q6LY81_METMP	Q6ly81 methanococc	973	79.5	5.7	485	2	Q73Y55_MYCPA	Q73y55 mycobacteri
901	80	5.7	409	2	Q4KKI5_PSEF5	Q4kki5 pseudomonas	974	79.5	5.7	492	2	Q5H3W7_XANOR	Q5h3w7 xanthomonas
902	80	5.7	429	1	ARSB_STAAU	P30329 staphylococ	975	79.5	5.7	499	2	Q9UYPI_PYRAB	Q9uypi pyrococcus
903	80	5.7	429	2	Q9AC73_STAAN	Q9ac73 staphylococ	976	79.5	5.7	500	2	Q4N1S4_THEPA	Q4nl84 theileria p
904	80	5.7	438	2	Q3F4D4_9BURK	Q3f4d4 burkholderi	977	79.5	5.7	505	2	Q93GK1_BACST	Q93gk1 bacillus st
905	80	5.7	439	2	Q8PGX4_XANAC	Q8pgx4 xanthomonas	978	79.5	5.7	515	2	Q2UCU8_ASPOR	Q2ucu8 aspergillus
906	80	5.7	445	2	Q6NF01_CORDI	Q6nf01 corynebacte	979	79.5	5.7	516	2	Q2IL18_9DELT	Q2il18 anaeromyxob
907	80	5.7	450	2	Q4MZY0_THEPA	Q4mzy0 theileria p	980	79.5	5.7	517	2	Q6MY57_ASPFU	Q6my57 aspergillus

981	79.5	5.7	527	2	Q440H4_SOLUS	Q440h4	solibacter	1054	79	5.7	377	2	Q9LXX8_ARATH	Q9lxx8	arabidopsis
982	79.5	5.7	535	2	Q4PKJ2_ORYSA	Q4pkj2	oryza sativ	1055	79	5.7	381	2	Q6FDD6_ACADI	Q6fdd6	acinetobact
983	79.5	5.7	539	1	FIXN_AGR7	P98055	agrobacteri	1056	79	5.7	386	2	Q7NCK9_GLOVI	Q7nck9	gloeobacter
984	79.5	5.7	542	2	Q2YKC6_BRUA2	Q2ykc6	brucella ab	1057	79	5.7	389	2	Q5L9Y3_BACFN	Q5l9y3	bacteroides
985	79.5	5.7	542	2	Q8FWF3_BRUSU	Q8fwf3	brucella su	1058	79	5.7	389	2	Q64Q89_BACFR	Q64q89	bacteroides
986	79.5	5.7	542	2	Q8YBW8_BRUME	Q8ybw8	brucella me	1059	79	5.7	390	2	Q9X158_THEME	Q9x158	thermotoga
987	79.5	5.7	542	2	Q577Q8_BRUAB	Q577q8	brucella ab	1060	79	5.7	395	1	HMEB_ARCFU	Q29750	archaeoglob
988	79.5	5.7	544	2	Q64940_9CORO	Q64940	infectious	1061	79	5.7	400	2	Q3XTS0_9PROT	Q3xts0	magnetococc
989	79.5	5.7	559	2	Q5L073_GEOKA	Q5l073	geobacillus	1062	79	5.7	405	2	Q2RNM4_RHORU	Q2rnm4	rhodospiril
990	79.5	5.7	563	2	Q2U9X1_ASPOR	Q2u9x1	aspergillus	1063	79	5.7	409	2	Q4IAN6_GIBZE	Q4ian6	giberella
991	79.5	5.7	566	2	Q5BGW2_EMENI	Q5bgw2	aspergillus	1064	79	5.7	409	2	Q6E830_9HEMI	Q6e830	potnia glad
992	79.5	5.7	566	2	Q5EQN7_9HYME	Q5eqn7	perga conde	1065	79	5.7	410	1	Y588_BUCAI	P57648	buchnera ap
993	79.5	5.7	570	2	Q8UF62_AGR75	Q8uf62	agrobacteri	1066	79	5.7	414	2	Q66R30_YEAST	Q66r30	saccharomyc
994	79.5	5.7	573	2	Q63FV4_BACCZ	Q63fv4	bacillus ce	1067	79	5.7	420	2	Q2RZ27_9SPHI	Q2rzz7	salinibacte
995	79.5	5.7	573	2	Q81V13_BACAN	Q81v13	bacillus an	1068	79	5.7	423	2	Q3Q6K6_9GAMM	Q3q6k6	shewanella
996	79.5	5.7	588	2	Q4I543_GIBZE	Q4i543	giberella	1069	79	5.7	429	2	Q63YG8_BURPS	Q63yg8	burkholderi
997	79.5	5.7	593	2	Q6BM61_DEBHA	Q6bm61	debaryomyce	1070	79	5.7	438	2	Q7ACT1_ECO57	Q7act1	escherichia
998	79.5	5.7	596	2	Q5Z6S8_ORYSA	Q5z6s8	oryza sativ	1071	79	5.7	438	2	Q8FGD5_ECOL6	Q8fgd5	escherichia
999	79.5	5.7	598	2	Q7CZ11_AGR75	Q7cz11	agrobacteri	1072	79	5.7	439	2	Q4WKR6_ASPFU	Q4wkr6	aspergillus
1000	79.5	5.7	600	2	Q6LKC0_PHOPR	Q6lkc0	photobacter	1073	79	5.7	442	2	Q4W667_VIBCH	Q4w667	vibrio chol
1001	79.5	5.7	603	2	Q33H54_METHU	Q33h54	methanospir	1074	79	5.7	443	2	Q6LKM2_PHOPR	Q6lkm2	photobacter
1002	79.5	5.7	613	2	Q8CEBQ1_MOUSE	Q8cbq1	mus musculus	1075	79	5.7	444	2	Q7WT98_BORPE	Q7vt98	bordetella
1003	79.5	5.7	628	2	Q67ML1_SYMTH	Q67ml1	symbiobacte	1076	79	5.7	444	2	Q7W2C1_BORPA	Q7w2c1	bordetella
1004	79.5	5.7	632	2	Q9AZ47_BPSP6	Q9az47	enterobacte	1077	79	5.7	444	2	Q7WR89_BORBR	Q7wr89	bordetella
1005	79.5	5.7	635	2	Q2RAP8_ORYSA	Q2rap8	oryza sativ	1078	79	5.7	444	2	Q9KKW1_VIBCH	Q9kkw1	vibrio chol
1006	79.5	5.7	639	2	Q5WC83_BACSK	Q5wc83	bacillus cl	1079	79	5.7	446	2	Q6L0U0_PICTO	Q6l0u0	microphilus
1007	79.5	5.7	643	2	Q2RU29_RHORU	Q2ru29	rhodospiril	1080	79	5.7	447	2	Q6GER0_STAAR	Q6ger0	staphylococ
1008	79.5	5.7	669	2	Q6USQ3_9DIPS	Q6usq3	valeriana e	1081	79	5.7	453	2	Q8Y8B8_LISMO	Q8y8b8	listeria mo
1009	79.5	5.7	677	2	Q6CY48_KLULA	Q6cy48	kluuveromyc	1082	79	5.7	456	2	Q9HID5_THEAC	Q9hid5	thermoplasm
1010	79.5	5.7	695	2	Q9TJS9_9GENT	Q9tjs9	mussaenda a	1083	79	5.7	456	2	Q7PB27_RICSI	Q7pb27	rickettsia
1011	79.5	5.7	697	1	HAK4_ORYSA	Q6ysa9	oryza sativ	1084	79	5.7	457	2	Q4N1S2_THEPA	Q4n1s2	theileria p
1012	79.5	5.7	699	2	Q91YL7_MOUSE	Q91yl7	mus musculus	1085	79	5.7	459	2	Q3BEP6_9FALC	Q3bep6	spizaetus n
1013	79.5	5.7	726	2	Q2ZK71_CALSA	Q2zk71	caldicellul	1086	79	5.7	464	2	Q8RC72_THETN	Q8rc72	thermoanaer
1014	79.5	5.7	733	2	Q44KZ0_CHRSL	Q44kz0	chromohalob	1087	79	5.7	465	2	Q44ON7_SOLUS	Q44on7	solibacter
1015	79.5	5.7	734	2	Q4RWS7_TETNG	Q4rws7	tetraodon n	1088	79	5.7	468	2	Q2QWH8_ORYSA	Q2qwh8	oryza sativ
1016	79.5	5.7	735	2	Q4DAB4_TRYCR	Q4dab4	trypanosoma	1089	79	5.7	473	2	Q16252_CABEL	Q16252	caenorhabdi
1017	79.5	5.7	741	2	Q32132_9ASTR	Q32132	chrysanthem	1090	79	5.7	477	2	Q3NNW8_9GAMM	Q3nnw8	shewanella
1018	79.5	5.7	831	1	SL9A3_RAT	P26433	rattus norv	1091	79	5.7	479	2	Q16926_CABEL	Q16926	caenorhabdi
1019	79.5	5.7	878	2	Q8MKL0_DROME	Q8mk10	drosophila	1092	79	5.7	481	2	Q62EY5_BURMA	Q62ey5	burkholderi
1020	79.5	5.7	890	2	Q2Y5X4_NITMU	Q2y5x4	nitrosospir	1093	79	5.7	489	2	Q97EE9_CLOAB	Q97ee9	clostridium
1021	79.5	5.7	976	2	Q96VU4_BLUGR	Q96vu4	blumeria gr	1094	79	5.7	491	2	Q4KH41_PSEF5	Q4kh41	pseudomonas
1022	79.5	5.7	1078	2	Q55F45_DICDI	Q55f45	dictyosteli	1095	79	5.7	492	2	Q5A405_CANAL	Q5a405	candida alb
1023	79.5	5.7	1163	2	Q2U2G2_ASPOR	Q2u2g2	aspergillus	1096	79	5.7	497	2	Q7TNN9_RAT	Q7tnn9	rattus norv
1024	79.5	5.7	1321	2	Q4RSL1_TETNG	Q4rs11	tetraodon n	1097	79	5.7	498	2	Q4X148_ASPFU	Q4x148	aspergillus
1025	79.5	5.7	1529	2	Q5HB09_EHRRW	Q5hb09	ehrlichia r	1098	79	5.7	501	2	Q5TMB6_CHICK	Q5tmb6	gallus gall
1026	79.5	5.7	1539	2	Q4UE92_THEAN	Q4ue92	theileria a	1099	79	5.7	517	2	Q9XYS3_DICDI	Q9xys3	dictyosteli
1027	79.5	5.7	1569	2	Q5FEL3_EHRRW	Q5fel3	ehrlichia r	1100	79	5.7	518	2	Q3CGR2_THBET	Q3cgr2	thermoanaer
1028	79.5	5.7	1591	2	Q5FFL1_EHRRG	Q5ffl1	ehrlichia r	1101	79	5.7	524	2	Q4WIS8_ASPFU	Q4wi58	aspergillus
1029	79	5.7	154	2	Q42211_NECMA	Q42211	necturus ma	1102	79	5.7	526	2	Q4J830_SULAC	Q4j830	sulfolobus
1030	79	5.7	172	1	NUG6_PETMA	Q35544	petromyzon	1103	79	5.7	534	2	Q88Z37_LACPL	Q88z37	lactobacill
1031	79	5.7	183	1	Y507_HAEIN	P44010	haemophilus	1104	79	5.7	545	2	Q35PX2_9BRAD	Q35px2	bradyrhizob
1032	79	5.7	183	2	Q4QN39_HAEI8	Q4qn39	haemophilus	1105	79	5.7	551	2	Q421G2_DESHA	Q421g2	desulfitoba
1033	79	5.7	192	2	Q6CYK5_ERWCT	Q6cyk5	erwinia car	1106	79	5.7	585	2	Q60UUI_CAEBR	Q60uu1	caenorhabdi
1034	79	5.7	226	2	Q6HCD0_BACHK	Q6hcd0	bacillus th	1107	79	5.7	595	2	Q837Q4_ENTFA	Q837q4	enterococcu
1035	79	5.7	229	2	Q8XIK9_CLOPE	Q8xik9	clostridium	1108	79	5.7	602	2	Q70XI8_9META	Q70xi8	rhyncholest
1036	79	5.7	248	2	Q50EH3_LACRE	Q50eh3	lactobacill	1109	79	5.7	657	2	Q3SUK6_NITWN	Q3suk6	nitrobacter
1037	79	5.7	269	2	Q3QSB7_9RHOB	Q3qsb7	silicibacte	1110	79	5.7	658	2	Q6XJH8_9ERIC	Q6xjh8	sideroxylon
1038	79	5.7	278	2	Q5K125_9ROSI	Q5k125	populus tre	1111	79	5.7	658	2	Q6XJL0_9ERIC	Q6xjl0	nesoluma po
1039	79	5.7	282	2	Q4ULV8_RICFE	Q4ulv8	rickettsia	1112	79	5.7	658	2	Q6XJ12_9ERIC	Q6xji2	sideroxylon
1040	79	5.7	289	2	Q946J9_MEDTR	Q946j9	medicago tr	1113	79	5.7	669	1	NU5M_ARATH	P29388	arabidopsis
1041	79	5.7	289	2	Q5U7L0_9FABA	Q5u7l0	glycyrrhiza	1114	79	5.7	682	2	Q69UI4_ORYSA	Q69ui4	oryza sativ
1042	79	5.7	293	1	Y543_CHLPN	Q9z809	chlamydia p	1115	79	5.7	685	2	Q19822_9LAMI	Q19822	alsobia sp.
1043	79	5.7	293	2	Q9KDZ5_BACHD	Q9kdz5	bacillus ha	1116	79	5.7	687	2	Q3HT37_9BORA	Q3ht37	tiqulia hi
1044	79	5.7	300	2	Q6HM61_BACHK	Q6hm61	bacillus th	1117	79	5.7	687	2	Q3HT35_9BORA	Q3ht35	tiqulia hi
1045	79	5.7	307	2	Q9JTO9_NEIMA	Q9jtg9	neisseria m	1118	79	5.7	688	2	Q8M8X1_9ASTE	Q8m8x1	sphenoclea
1046	79	5.7	310	2	Q7MJN1_VIBVY	Q7mjn1	vibrio vuln	1119	79	5.7	692	2	Q35193_MOUSE	Q35193	mus musculu
1047	79	5.7	310	2	Q8DAH5_VIBVU	Q8dah5	vibrio vuln	1120	79	5.7	723	2	Q9TIW2_9ASTE	Q9tiw2	phacelia ca
1048	79	5.7	322	2	Q5PLX1_AZOSE	Q5ply1	azoarcus sp	1121	79	5.7	738	2	Q9TJS8_MORCI	Q9tjs8	morinda cit
1049	79	5.7	341	2	Q2QWH7_ORYSA	Q2qwh7	oryza sativ	1122	79	5.7	746	2	Q9TLB7_DIGPU	Q9tlb7	digitalis p
1050	79	5.7	354	2	Q97C19_THEVO	Q97c19	thermoplasm	1123	79	5.7	758	2	Q40R23_DESAC	Q40r23	desulfuromo
1051	79	5.7	369	2	Q8PL40_XANAC	Q8pl40	xanthomonas	1124	79	5.7	819	2	Q31582_BACSU	Q31582	bacillus su
1052	79	5.7	372	2	Q6GIA8_STAAR	Q6gia8	staphylococ	1125	79	5.7	830	2	Q2V621_CANAL	Q2v621	candida alb
1053	79	5.7	373	2	Q8LBH3_ARATH	Q8lbh3	arabidopsis	1126	79	5.7	1046	2	Q2X4H3_9GAMM	Q2x4h3	shewanella

1127	79	5.7	1067	2	Q3Q8Y9_9GAMM	Q3q8y9 shewanella	1200	78.5	5.6	474	2	Q4QK73_HAE18	Q4qk73 haemophilus
1128	79	5.7	1068	2	Q2ZNP8_SHEPU	Q2znp8 shewanella	1201	78.5	5.6	475	2	Q49VD6_STAS1	Q49vd6 staphylococ
1129	79	5.7	1166	2	Q44EW7_CHRSL	Q44ew7 chromohalob	1202	78.5	5.6	478	2	Q5AY52_EMENI	Q5ay52 aspergillus
1130	79	5.7	1501	2	Q8CIQ9_MOUSE	Q8ciq9 mus musculu	1203	78.5	5.6	479	2	Q5GCA8_RHOGE	Q5gca8 rhodocycilus
1131	79	5.7	1521	2	Q3TDN0_MOUSE	Q3tdn0 mus musculu	1204	78.5	5.6	482	2	Q83AQ0_COXBU	Q83aq0 coxiella bu
1132	79	5.7	1521	2	Q3UUL8_MOUSE	Q3uul8 mus musculu	1205	78.5	5.6	483	2	Q85MF7_9NEOP	Q85mf7 cyrestis th
1133	79	5.7	1521	2	Q8OZ28_MOUSE	Q8oz28 mus musculu	1206	78.5	5.6	483	2	Q2LB19_9NEOP	Q2lbi9 thauria ali
1134	79	5.7	1521	2	Q8CGS3_MOUSE	Q8cgs3 mus musculu	1207	78.5	5.6	487	2	Q3ZEF8_EPIFL	Q3zef8 epidermophy
1135	79	5.7	1521	2	Q8CIP6_MOUSE	Q8cip6 mus musculu	1208	78.5	5.6	493	2	Q9VOT0_PYRAB	Q9vot0 pyrococcus
1136	79	5.7	1709	2	Q6LIW5_CAEBR	Q6liw5 caenorhabdi	1209	78.5	5.6	501	2	Q8FB10_ECOL6	Q8fb10 escherichia
1137	79	5.7	1794	2	Q4QGV5_LEIMA	Q4ggv5 leishmania	1210	78.5	5.6	502	2	Q3GYP4_9ACTO	Q3gyp4 nocardioide
1138	79	5.7	2198	2	Q18990_CAEEL	Q18990 caenorhabdi	1211	78.5	5.6	505	2	Q3ICQ3_PSEHT	Q3icq3 pseudoalter
1139	78.5	5.6	169	2	Q1HSA7_HALSA	Q1hsa7 halobacteri	1212	78.5	5.6	510	2	Q9B8Y2_FASHE	Q9b8y2 fasciola he
1140	78.5	5.6	182	2	Q3CSW3_ALTAT	Q3csw3 pseudoalter	1213	78.5	5.6	512	2	Q6ZMD2_HUMAN	Q6zmd2 homo sapien
1141	78.5	5.6	188	2	Q493Y2_BLOPB	Q493y2 blochmannia	1214	78.5	5.6	518	2	Q3VHK6_9SPHN	Q3vhk6 sphingopyxi
1142	78.5	5.6	241	1	MCBE_ECOLI	P05528 escherichia	1215	78.5	5.6	526	2	Q6MUB7_MYCMS	Q6mub7 mycoplasma
1143	78.5	5.6	242	2	Q6LFC6_PHOPR	Q6lpc6 photobacter	1216	78.5	5.6	536	2	Q2U3S4_ASPOR	Q2u3s4 aspergillus
1144	78.5	5.6	247	2	Q3B7R3_BRARE	Q3b7r3 brachydanio	1217	78.5	5.6	554	2	Q2W3Z5_MAGSA	Q2w3z5 magnetospir
1145	78.5	5.6	254	2	Q4SVF4_TETNG	Q4svf4 tetraodon n	1218	78.5	5.6	559	2	Q6DCE3_XENLA	Q6dce3 xenopus lae
1146	78.5	5.6	259	2	Q3CMD0_ALTAT	Q3cmd0 pseudoalter	1219	78.5	5.6	574	2	Q3SON5_RALME	Q3son5 ralstonia m
1147	78.5	5.6	264	2	Q6ITH4_CERBA	Q6ith4 cercaria ba	1220	78.5	5.6	579	2	Q5O465_MYCTU	Q5o465 mycobacteri
1148	78.5	5.6	264	2	Q6ITI2_CERBA	Q6iti2 cercaria ba	1221	78.5	5.6	580	2	Q4MPJ8_BACCE	Q4mpj8 bacillus ce
1149	78.5	5.6	281	2	Q5UJ71_PYRKO	Q5jj71 pyrococcus	1222	78.5	5.6	583	2	Q950T2_HYACU	Q950t2 hyaloraphid
1150	78.5	5.6	293	2	Q4W8E1_9ACAR	Q4w8e1 leptotrombi	1223	78.5	5.6	591	2	Q8SXJ9_DROME	Q8sxj9 drosophila
1151	78.5	5.6	298	2	Q65V25_MANSM	Q65v25 mannheimia	1224	78.5	5.6	591	2	Q9V9U1_DROME	Q9v9u1 drosophila
1152	78.5	5.6	298	2	Q73T54_MYCPA	Q73t54 mycobacteri	1225	78.5	5.6	609	2	Q2Y4R6_9ARCH	Q2y4r6 uncultured
1153	78.5	5.6	302	2	Q4L8C2_STAHI	Q4l8c2 staphylococ	1226	78.5	5.6	620	2	Q2TK00_9ERIC	Q2tk00 pelletiera
1154	78.5	5.6	314	2	Q970C7_SULTO	Q970c7 sulfolobus	1227	78.5	5.6	622	1	COX1_BACSU	P24010 bacillus su
1155	78.5	5.6	316	2	Q7EY23_ORYSA	Q7eyz3 oryza sativ	1228	78.5	5.6	624	2	Q9LYR6_ARATH	Q9lyr6 arabidopsis
1156	78.5	5.6	320	2	Q9BBU4_9MYRT	Q9bbu4 warneckea m	1229	78.5	5.6	634	2	Q3VQ16_9CHLB	Q3vq16 pelodictyon
1157	78.5	5.6	320	2	Q7ZWS9_XENLA	Q7zws9 xenopus lae	1230	78.5	5.6	641	2	Q5NM95_ZYMMO	Q5nm95 zymomonas m
1158	78.5	5.6	321	2	Q9BBV9_9MYRT	Q9bbv9 mouriri hel	1231	78.5	5.6	652	2	Q9TIX1_9ASTE	Q9tix1 codon schen
1159	78.5	5.6	324	2	Q2IVA0_RHOPA	Q2iva0 rhodopseudo	1232	78.5	5.6	682	2	Q6USQ0_9DIPS	Q6usq0 valeriana c
1160	78.5	5.6	324	2	Q5P546_NEIG1	Q5f546 neisseria g	1233	78.5	5.6	686	2	Q3HT46_9BORA	Q3ht46 tiquilia gr
1161	78.5	5.6	325	2	Q9MRZ1_9MYRT	Q9mrz1 heterocentr	1234	78.5	5.6	691	2	Q93YK5_BRANA	Q93yk5 brassica na
1162	78.5	5.6	330	2	Q9VU64_DROME	Q9vu64 drosophila	1235	78.5	5.6	699	2	Q2LYT2_DROPS	Q2lyt2 drosophila
1163	78.5	5.6	333	2	Q3D8R7_STRAG	Q3d8r7 streptococc	1236	78.5	5.6	732	2	Q98707_9GENT	Q98707 mussaenda e
1164	78.5	5.6	333	2	Q3DEQ3_STRAG	Q3deg3 streptococc	1237	78.5	5.6	732	2	Q9TJP6_9GENT	Q9tjp6 strumpfia m
1165	78.5	5.6	333	2	Q3KOB7_STRAI	Q3kob7 streptococc	1238	78.5	5.6	734	2	Q9TJQ0_9GENT	Q9tjq0 rogiera suf
1166	78.5	5.6	340	2	Q8G845_BIFLO	Q8g845 bifidobacte	1239	78.5	5.6	744	2	Q32645_MENTR	Q32645 menyanthes
1167	78.5	5.6	356	2	Q8DTT2_STRMU	Q8dtt2 streptococc	1240	78.5	5.6	779	2	Q6A6U5_PROAC	Q6a6u5 propionibac
1168	78.5	5.6	362	2	Q3R3B4_XYLFA	Q3r3b4 xylella fas	1241	78.5	5.6	798	2	Q2KGF8_MAGGR	Q2kgf8 magnaporthe
1169	78.5	5.6	366	1	Y1196_METJA	Q58596 methanococc	1242	78.5	5.6	803	2	Q3FZU0_9DELT	Q3fzu0 pelobacter
1170	78.5	5.6	384	2	Q3CNM8_ALTAT	Q3cnm8 pseudoalter	1243	78.5	5.6	825	2	Q6N2I5_RHOPA	Q6n2i5 rhodopseudo
1171	78.5	5.6	389	2	Q4ZWE3_PSEU2	Q4zwe3 pseudomonas	1244	78.5	5.6	829	2	Q46G21_METBA	Q46g21 methanosarc
1172	78.5	5.6	389	2	Q93TD9_PSEYM	Q93td9 pseudomonas	1245	78.5	5.6	863	2	Q92L62_RHIME	Q92l62 rhizobium m
1173	78.5	5.6	389	2	Q87WD8_PSESM	Q87wd8 pseudomonas	1246	78.5	5.6	864	2	Q4L5U5_STAHI	Q4l5u5 staphylococ
1174	78.5	5.6	393	2	Q639K7_BACCZ	Q639k7 bacillus ce	1247	78.5	5.6	898	2	Q5I5C8_9TELE	Q5i5c8 cyprinid sp
1175	78.5	5.6	395	2	Q612Y3_CAEBR	Q612y3 caenorhabdi	1248	78.5	5.6	930	2	Q4E2X6_TRYCR	Q4e2x6 trypanosoma
1176	78.5	5.6	397	2	Q8KW37_9RHOB	Q8kw37 ruegeria sp	1249	78.5	5.6	1093	2	Q84W30_ARATH	Q84w30 arabidopsis
1177	78.5	5.6	397	2	Q5NHL1_FRATT	Q5nhl1 francisella	1250	78.5	5.6	1289	2	Q7RKA2_PLAYO	Q7rka2 plasmodium
1178	78.5	5.6	405	2	Q9U2M5_CAEEL	Q9u2m5 caenorhabdi	1251	78.5	5.6	1325	2	Q64533_ARATH	Q64533 arabidopsis
1179	78.5	5.6	411	2	Q2JKD1_9CYAN	Q2jkd1 cyanobacter	1252	78.5	5.6	2556	2	Q9QH56_9ALPH	Q9qh56 gallid herp
1180	78.5	5.6	411	2	Q89ZC7_BACTN	Q89zc7 bacteroides	1253	78.5	5.6	3172	2	Q4QAV5_LEIMA	Q4qav5 leishmania
1181	78.5	5.6	412	2	Q2MGY8_STAAN	Q2mgy8 staphylococ	1254	78.5	5.6	4856	2	Q7PZB3_ANOGA	Q7pzb3 anopheles g
1182	78.5	5.6	412	2	Q7A856_STAAN	Q7a856 staphylococ	1255	78	5.6	158	2	Q9XW23_CAEEL	Q9xw23 caenorhabdi
1183	78.5	5.6	412	2	Q99X84_STAAM	Q99x84 staphylococ	1256	78	5.6	197	2	Q98CZ0_RHILO	Q98cz0 rhizobium l
1184	78.5	5.6	414	2	Q4CWZ9_TRYCR	Q4cwz9 trypanosoma	1257	78	5.6	205	2	Q5VWV8_HUMAN	Q5vww8 homo sapien
1185	78.5	5.6	419	2	Q3PID7_9GAMM	Q3pid7 shewanella	1258	78	5.6	209	2	Q54NB5_DICDI	Q54nb5 dictyosteli
1186	78.5	5.6	436	2	Q4K6F5_PSEF5	Q4k6f5 pseudomonas	1259	78	5.6	227	2	Q8HMJ0_9TELE	Q8hmj0 carapus ber
1187	78.5	5.6	437	2	Q31IW2_THICR	Q31iw2 thiomicrosp	1260	78	5.6	231	2	Q5BL33_BRARE	Q5bl33 brachydanio
1188	78.5	5.6	438	2	Q4BIS3_PSE14	Q4bis3 pseudomonas	1261	78	5.6	261	2	Q33X10_9GAMM	Q33x10 shewanella
1189	78.5	5.6	442	2	Q2L207_BORAV	Q2l207 bordetella	1262	78	5.6	262	2	Q98A38_RHILO	Q98a38 rhizobium l
1190	78.5	5.6	443	2	Q57JM1_SALCH	Q57jm1 salmonella	1263	78	5.6	263	2	Q2S8N7_9GAMM	Q2s8n7 hahella che
1191	78.5	5.6	443	2	Q8ZLM4_SALTY	Q8zlw4 salmonella	1264	78	5.6	268	2	Q6LZZ9_METMP	Q6lzz9 methanococc
1192	78.5	5.6	447	2	Q6CYW0_ERWCT	Q6cyw0 erwinia car	1265	78	5.6	295	2	Q6P8F8_XENTR	Q6p8f8 xenopus tro
1193	78.5	5.6	457	2	Q410S4_KINRA	Q410s4 kinococcus	1266	78	5.6	299	2	Q9QX34_MOUSE	Q9qx34 mus musculu
1194	78.5	5.6	458	2	Q4HHT9_CAMCO	Q4hht9 campylobact	1267	78	5.6	307	2	Q9JYR8_NEIMB	Q9jyr8 neisseria m
1195	78.5	5.6	464	2	Q979J8_THEVO	Q979j8 thermoplasm	1268	78	5.6	327	2	Q974Q0_SULTO	Q974q0 sulfolobus
1196	78.5	5.6	470	2	Q6C8J1_YARLI	Q6c8j1 yarrowia li	1269	78	5.6	331	2	Q5JYAI_HUMAN	Q5jyal homo sapien
1197	78.5	5.6	470	2	Q31KW0_SYNPF	Q31kw0 synecococc	1270	78	5.6	335	1	MRAY_CHLMU	Q9plg6 chlamydia m
1198	78.5	5.6	470	2	Q5N109_SYNPF	Q5n109 synecococc	1271	78	5.6	335	2	Q41WK3_DESHA	Q41wk3 desulfitoba
1199	78.5	5.6	471	2	Q6AB86_PROAC	Q6ab86 propionibac	1272	78	5.6	338	2	Q9KY69_STRCO	Q9ky69 streptomyce



1273	78	5.6	340	2	Q7S3I4_NEUCR	Q7s3i4 neurospora	1346	78	5.6	834	2	Q8E9A7_SHEON	Q8e9a7 shewanella
1274	78	5.6	353	2	Q8Q0J7_METMA	Q8q0j7 methanosarc	1347	78	5.6	1087	2	Q2K2Z3_RHIET	Q2k2z3 rhizobium e
1275	78	5.6	358	2	Q3CEJ9_THEET	Q3cej9 thermoaer	1348	78	5.6	1533	2	Q4YU69_PLABE	Q4yu69 leishmania
1276	78	5.6	366	2	Q6SF48_BACLD	Q6sf48 bacillus li	1349	77.5	5.6	199	2	Q4QEX1_LEIMA	Q4qex1 leishmania
1277	78	5.6	379	2	Q85L69_9TREM	Q85l69 chimaerohem	1350	77.5	5.6	206	2	Q5KYI9_GEOKA	Q5kyi9 geobacillus
1278	78	5.6	382	2	Q92IS9_RICCN	Q92is9 rickettsia	1351	77.5	5.6	212	2	Q9KAJ4_BACHD	Q9kaj4 bacillus ha
1279	78	5.6	386	2	Q5P1K0_AZOSE	Q5p1k0 azoarcus sp	1352	77.5	5.6	229	1	YR809_MIMIV	Q5uqi2 mimivirus
1280	78	5.6	388	2	Q9RTZ5_DEIRA	Q9rtz5 deinococcus	1353	77.5	5.6	243	2	Q93RC4_ECOLI	Q93rc4 escherichia
1281	78	5.6	392	2	Q9ESM5_RAT	Q9esm5 rattus norv	1354	77.5	5.6	245	2	Q3HI18_TRIER	Q3hil8 trichodesmi
1282	78	5.6	396	2	Q57MB7_SALCH	Q57mb7 salmonella	1355	77.5	5.6	248	2	Q3VHY8_9CHLB	Q3vhy8 pelodictyon
1283	78	5.6	396	2	Q5PE30_SALPA	Q5pe30 salmonella	1356	77.5	5.6	256	2	Q3IDA4_PSEHT	Q3ida4 pseudoalter
1284	78	5.6	396	2	Q8ZNJ7_SALTY	Q8znj7 salmonella	1357	77.5	5.6	260	2	Q7VV38_BORPE	Q7vv38 bordetella
1285	78	5.6	396	2	Q8Z581_SALTI	Q8z581 salmonella	1358	77.5	5.6	260	2	Q7W0U7_BORPA	Q7w0u7 bordetella
1286	78	5.6	408	2	Q81RH3_BACAN	Q81rh3 bacillus an	1359	77.5	5.6	260	2	Q7WN67_BORBR	Q7wn67 bordetella
1287	78	5.6	409	1	KCNK3_MOUSE	Q35l11 mus musculu	1360	77.5	5.6	268	2	Q8U2B7_PYRFU	Q8u2b7 pyrococcus
1288	78	5.6	409	2	Q6HZP9_BACAN	Q6hzp9 bacillus an	1361	77.5	5.6	276	2	Q4CXM5_TRYCR	Q4cxm5 trypanosoma
1289	78	5.6	409	2	Q6HJQ7_BACHK	Q6hjq7 bacillus th	1362	77.5	5.6	283	2	Q92WH1_RHIME	Q92wh1 rhizobium m
1290	78	5.6	411	1	KCNK3_RAT	Q54912 rattus norv	1363	77.5	5.6	287	2	Q6NJG1_CORDI	Q6njg1 corynebacte
1291	78	5.6	414	1	YM87_YEAST	Q04835 saccharomyc	1364	77.5	5.6	288	2	Q9MF61_BETVU	Q9mf61 beta vulgar
1292	78	5.6	415	2	Q35XX3_9GAMM	Q35xx3 shewanella	1365	77.5	5.6	288	2	Q9M4S9_ALLCE	Q9m4s9 allium cepa
1293	78	5.6	416	1	OX1R_MOUSE	P58307 mus musculu	1366	77.5	5.6	288	2	Q3B0R8_SYNS9	Q3b0r8 synechococc
1294	78	5.6	416	2	Q5FLR6_LACAC	Q5flr6 lactobacill	1367	77.5	5.6	291	2	Q4HPK2_CAMUP	Q4hpk2 campylobact
1295	78	5.6	421	2	Q22672_CAEEL	Q22672 caenorhabdi	1368	77.5	5.6	291	2	Q6ASD9_DESPS	Q6asd9 desulfotale
1296	78	5.6	424	2	Q6SFZ8_9BACT	Q6sfz8 uncultured	1369	77.5	5.6	292	2	Q4EKI1_LISMO	Q4ekil listeria mo
1297	78	5.6	427	2	Q421Y0_DESHA	Q421y0 desulfitoba	1370	77.5	5.6	292	2	Q8Y8N6_LISMO	Q8y8n6 listeria mo
1298	78	5.6	428	2	Q6LS34_PHOPR	Q6ls34 photobacter	1371	77.5	5.6	292	2	Q721V7_LISMP	Q721v7 listeria mo
1299	78	5.6	429	2	Q4LAB4_STAHTJ	Q4lab4 staphylococ	1372	77.5	5.6	293	2	Q2XBL5_PSEPU	Q2xbl5 pseudomonas
1300	78	5.6	449	2	Q4HES6_CAMCO	Q4hes6 campylobact	1373	77.5	5.6	293	2	Q88E98_PSEPK	Q88e98 pseudomonas
1301	78	5.6	449	2	Q4HIV2_CAMLA	Q4hiv2 campylobact	1374	77.5	5.6	293	2	Q8ZGV5_YERPE	Q8zgv5 yersinia pe
1302	78	5.6	452	2	Q7VAQ3_PROMA	Q7vaq3 prochloroco	1375	77.5	5.6	296	2	Q33U75_9GAMM	Q33u75 shewanella
1303	78	5.6	459	2	Q3BEN3_9FALC	Q3ben3 spizaetus a	1376	77.5	5.6	296	2	Q92ZHO_RHIME	Q92zh0 rhizobium m
1304	78	5.6	462	2	Q9Y8L1_PYRFU	Q9y8l1 pyrococcus	1377	77.5	5.6	297	2	Q2JX36_9CYAN	Q2jx36 cyanobacter
1305	78	5.6	467	2	Q95JD3_RABIT	Q95jd3 oryctolagus	1378	77.5	5.6	300	2	Q31U75_SHIBS	Q31u75 shigella bo
1306	78	5.6	470	2	Q3JCK0_NITOC	Q3jck0 nitrosococc	1379	77.5	5.6	308	2	Q660J1_BORGA	Q660j1 borrelia ga
1307	78	5.6	474	2	Q3XX38_ENTFC	Q3xx38 enterococcu	1380	77.5	5.6	312	2	Q7TR57_MOUSE	Q7tr57 mus musculu
1308	78	5.6	474	2	Q8GGM7_STRAZ	Q8ggm7 streptomyce	1381	77.5	5.6	312	2	Q8VG20_MOUSE	Q8vg20 mus musculu
1309	78	5.6	476	2	Q2WYS7_9GAMM	Q2wys7 shewanella	1382	77.5	5.6	313	2	Q7TS53_MOUSE	Q7ts53 mus musculu
1310	78	5.6	484	2	Q33J33_METHU	Q33j33 methanospir	1383	77.5	5.6	317	2	Q8RFJ5_FUSNN	Q8rfj5 fusobacteri
1311	78	5.6	486	2	Q8EKR6_SHEON	Q8ekr6 shewanella	1384	77.5	5.6	318	1	NULM_VARRU	Q94vc3 varanus rud
1312	78	5.6	486	2	Q687I4_MOUSE	Q687i4 mus musculu	1385	77.5	5.6	321	2	Q94VI2_VARGI	Q94vi2 varanus g1g
1313	78	5.6	490	2	Q8FP18_COREF	Q8fp18 corynebacte	1386	77.5	5.6	327	2	Q9MRZ6_9MYRT	Q9mrz6 comolia cor
1314	78	5.6	495	2	Q6R9L4_MAIZE	Q6r9l4 zea mays (m	1387	77.5	5.6	333	2	Q3D2E9_STRAG	Q3d2e9 streptococc
1315	78	5.6	498	2	Q8BVS0_MOUSE	Q8bvs0 mus musculu	1388	77.5	5.6	335	2	Q9X0N3_THEMA	Q9x0n3 thermotoga
1316	78	5.6	511	2	Q2JPR0_9CYAN	Q2jpr0 cyanobacter	1389	77.5	5.6	347	2	Q70RW1_9CETA	Q70rw1 berardius b
1317	78	5.6	517	2	Q98H22_RHILO	Q98h22 rhizobium l	1390	77.5	5.6	354	2	Q2UTW7_ASPOR	Q2utw7 aspergillus
1318	78	5.6	521	2	Q3QE78_9GAMM	Q3qe78 shewanella	1391	77.5	5.6	359	2	Q38FV3_9TRYYP	Q38fv3 trypanosoma
1319	78	5.6	526	2	Q47B84_DECAR	Q47b84 dechloromon	1392	77.5	5.6	359	2	Q6GDS8_STAAR	Q6gds8 staphylococ
1320	78	5.6	533	2	Q35HA8_9BRAD	Q35ha8 bradyrhizob	1393	77.5	5.6	363	2	Q9YFU4_AERPE	Q9yfu4 aeropyrum p
1321	78	5.6	537	2	Q3JX86_BURP1	Q3jx86 bruckholderi	1394	77.5	5.6	367	2	Q67RR1_SYNTH	Q67rr1 symbiobacte
1322	78	5.6	538	2	Q9JAE1_9PARA	Q9jae1 mumps virus	1395	77.5	5.6	368	2	Q85GB7_9DIPS	Q85gb7 cryptothlad
1323	78	5.6	540	2	Q54IV7_DICDI	Q54iv7 dictyosteli	1396	77.5	5.6	370	2	Q4D715_TRYCR	Q4d715 trypanosoma
1324	78	5.6	551	2	Q8BWG6_MOUSE	Q8bwg6 m 0 day neo	1397	77.5	5.6	372	2	Q5AQX4_EMENI	Q5aqx4 aspergillus
1325	78	5.6	553	2	Q6CQ66_KLULA	Q6cq66 kluyveromyc	1398	77.5	5.6	386	2	Q4ZR77_PSEU2	Q4zr77 pseudomonas
1326	78	5.6	554	2	Q34FM4_RHOPA	Q34fm4 rhodopseudo	1399	77.5	5.6	386	2	Q3SHL0_THIDA	Q3shl0 thiobacillu
1327	78	5.6	554	2	Q6NAP5_RHOPA	Q6nap5 rhodopseudo	1400	77.5	5.6	389	2	Q3QE50_9GAMM	Q3qe50 shewanella
1328	78	5.6	560	2	Q467V6_METBA	Q467v6 methanosarc	1401	77.5	5.6	398	2	Q57PC1_SALCH	Q57pci salmonella
1329	78	5.6	565	2	Q9F3S8_RHOMR	Q9f3s8 rhodothermu	1402	77.5	5.6	399	2	Q978I2_THEVO	Q978i2 thermoplasma
1330	78	5.6	573	2	Q721X4_LEPIC	Q721x4 leptospira	1403	77.5	5.6	406	2	Q6DNG7_SOYBN	Q6dng7 glycine max
1331	78	5.6	574	2	Q72T06_LEPIC	Q72t06 leptospira	1404	77.5	5.6	406	2	Q4JZ96_STRPN	Q4jz96 streptococc
1332	78	5.6	574	2	Q8F2F8_LEPIN	Q8f2f8 leptospira	1405	77.5	5.6	425	2	Q3GKD4_CHLVI	Q3gkd4 prosthecoch
1333	78	5.6	581	2	Q59TM8_CANAL	Q59tm8 candida alb	1406	77.5	5.6	436	2	Q6P6X7_BRARE	Q6p6x7 brachydanio
1334	78	5.6	581	2	Q59TR0_CANAL	Q59tr0 candida alb	1407	77.5	5.6	438	2	Q33TM7_9GAMM	Q33tm7 shewanella
1335	78	5.6	585	2	Q59MN0_CANAL	Q59mn0 candida alb	1408	77.5	5.6	443	2	Q8TRL4_METAC	Q8trl4 methanosarc
1336	78	5.6	587	2	Q4ZL77_PSEU2	Q4zl77 pseudomonas	1409	77.5	5.6	446	2	Q4NIJ1_9MICC	Q4ni11 arthrobacte
1337	78	5.6	650	2	Q01843_CAEEL	Q01843 caenorhabdi	1410	77.5	5.6	448	2	Q2UR20_ASPOR	Q2urz0 aspergillus
1338	78	5.6	658	2	Q6XJL1_9ERIC	Q6xjl1 neolemonnie	1411	77.5	5.6	448	2	Q9XMU9_TETPY	Q9xmu9 tetrahymena
1339	78	5.6	659	2	Q5JB71_9ASPA	Q5jb71 babiana muc	1412	77.5	5.6	453	2	Q3CX85_ALTAT	Q3cx85 pseudoalter
1340	78	5.6	662	2	Q4K7U5_PSEF5	Q4k7u5 pseudomonas	1413	77.5	5.6	458	2	Q6CZJ3_ERWCT	Q6czj3 erwinia car
1341	78	5.6	672	2	Q5JBA6_9ASPA	Q5jba6 scadoxus ci	1414	77.5	5.6	459	2	Q85UJ5_COTCH	Q85uj5 coturnix ch
1342	78	5.6	694	2	Q4P677_SOLDU	Q4p677 solanum dul	1415	77.5	5.6	460	2	Q7N370_PHOLL	Q7n370 photorhabdu
1343	78	5.6	806	2	Q9P678_USDMA	Q9p678 ustilago ma	1416	77.5	5.6	461	2	Q8X7F9_ECO57	Q8x7f9 escherichia
1344	78	5.6	808	2	Q50V14_ENTHI	Q50v14 entamoeba h	1417	77.5	5.6	464	2	Q9I6G9_PSEAE	Q9i6g9 pseudomonas
1345	78	5.6	830	2	Q8PQA8_XANAC	Q8pga8 xanthomonas	1418	77.5	5.6	472	2	Q2WRP4_CLOBE	Q2wrp4 clostridium



1419	77.5	5.6	477	2	Q7MKV7_VIBVY	Q7mkv7 vibrio vuln
1420	77.5	5.6	477	2	Q87PF8_VIBPA	Q87pf8 vibrio para
1421	77.5	5.6	477	2	Q8D9I1_VIBVU	Q8d9i1 vibrio vuln
1422	77.5	5.6	479	2	Q7AEJ3_ECO57	Q7aej3 escherichia
1423	77.5	5.6	481	2	Q3QNW1_9RHOB	Q3gnw1 silicibacte
1424	77.5	5.6	481	2	Q2SJS3_9GAMM	Q2sjs3 habella che
1425	77.5	5.6	482	2	Q5KYK3_GEOKA	Q5kyk3 geobacillus
1426	77.5	5.6	483	2	Q2UOJ8_ASPOR	Q2uoj8 aspergillus
1427	77.5	5.6	484	2	Q4CDC2_CLOTR	Q4cdc2 clostridium
1428	77.5	5.6	492	2	Q7VFT5_HELHP	Q7vft5 helicobacte
1429	77.5	5.6	499	2	Q57JZ0_SALCH	Q57jz0 salmonella
1430	77.5	5.6	499	2	Q8Z3S3_SALTI	Q8z3s3 salmonella
1431	77.5	5.6	500	2	Q2K5A6_RHIET	Q2k5a6 rhizobium e
1432	77.5	5.6	504	2	Q688L6_ORYSA	Q688l6 oryza sativ
1433	77.5	5.6	507	2	Q7VSQ9_BORPE	Q7vsg9 bordetella
1434	77.5	5.6	507	2	Q7WDH8_BORBR	Q7wdh8 bordetella
1435	77.5	5.6	510	1	Y382_RICPR	Q9zde9 rickettsia
1436	77.5	5.6	510	2	Q9LE20_ARATH	Q9le20 arabidopsis
1437	77.5	5.6	510	2	Q4MX86_BACCE	Q4mx86 bacillus ce
1438	77.5	5.6	513	2	Q9KLS4_VIBCH	Q9kls4 vibrio chol
1439	77.5	5.6	520	2	Q32477_JUSAM	Q32477 justicia am
1440	77.5	5.6	524	2	Q458G9_9BURK	Q458g9 burkholderi
1441	77.5	5.6	524	2	Q4LPV5_9BURK	Q4lpv5 burkholderi
1442	77.5	5.6	526	1	STP13_ARATH	Q94az2 arabidopsis
1443	77.5	5.6	526	2	Q55WR7_CRYNE	Q55wr7 cryptococcu
1444	77.5	5.6	526	2	Q5KJ10_CRYNE	Q5kji0 cryptococcu
1445	77.5	5.6	527	2	Q5ATG4_EMENI	Q5atg4 aspergillus
1446	77.5	5.6	531	2	Q6YQU3_ONYPE	Q6yqu3 onion yello
1447	77.5	5.6	532	1	COX1_RHOCA	P98059 rhodobacter
1448	77.5	5.6	532	2	Q4OHU4_9RHOB	Q40hu4 jannaschia
1449	77.5	5.6	535	2	Q55577_SYNY3	Q55577 synchocyst
1450	77.5	5.6	538	2	Q43ZK5_SOLUS	Q43zk5 solibacter
1451	77.5	5.6	612	2	Q76HH6_KATPE	Q76hh6 katsuwonus
1452	77.5	5.6	612	2	Q85UE1_9SCOM	Q85ue1 euthynnus a
1453	77.5	5.6	616	2	Q3XM94_9PROT	Q3xm94 magnetococc
1454	77.5	5.6	617	2	Q7S080_NEUCR	Q7s080 neurospora
1455	77.5	5.6	630	1	SC6A4_MACMU	Q9myx0 macaca mula
1456	77.5	5.6	635	2	Q9AS57_ARATH	Q9ass7 arabidopsis
1457	77.5	5.6	639	2	Q85L86_PISOC	Q85l86 pisaster oc
1458	77.5	5.6	643	2	Q385G4_9TRYCP	Q385g4 trypanosoma
1459	77.5	5.6	648	2	Q8SLR2_COUGP	Q8slr2 couroupita
1460	77.5	5.6	649	2	Q28449_ARCFU	Q28449 archaeoglob
1461	77.5	5.6	660	2	Q6Y1T3_9LILI	Q6y1t3 lachnanthus
1462	77.5	5.6	665	2	Q9GGT9_9POAL	Q9ggt9 thermophilum a
1463	77.5	5.6	695	2	Q97A18_THEVA	Q97a18 thermoplasm
1464	77.5	5.6	698	2	Q6BG22_DEBHA	Q6bgz2 debaryomyce
1465	77.5	5.6	699	2	Q7VM04_9SOLA	Q7ym04 metternichi
1466	77.5	5.6	706	2	Q6MK05_BDEBA	Q6mk05 bdellovibri
1467	77.5	5.6	717	1	PAL2_ARATH	P45724 arabidopsis
1468	77.5	5.6	750	2	Q93S90_XANCP	Q93s90 xanthomonas
1469	77.5	5.6	776	2	Q61N20_CAEBR	Q61nz0 caenorhabdi
1470	77.5	5.6	821	2	Q4CY87_TRYCR	Q4cy87 trypanosoma
1471	77.5	5.6	839	2	Q8QTQ4_METAC	Q8qtq4 methanosarc
1472	77.5	5.6	855	2	Q75AV9_ASHGO	Q75av9 ashbya goss
1473	77.5	5.6	861	2	Q89FW4_BRAJA	Q89fw4 bradyrhizob
1474	77.5	5.6	870	1	GP155_HUMAN	Q7z3f1 homo sapien
1475	77.5	5.6	870	2	Q4G0Y6_HUMAN	Q4g0y6 homo sapien
1476	77.5	5.6	877	2	Q2SB79_9GAMM	Q2sb79 habella che
1477	77.5	5.6	881	2	Q3ILG1_PSEHT	Q3ilg1 pseudoalter
1478	77.5	5.6	945	1	SVI_AC1AD	Q6fg02 acinetobact
1479	77.5	5.6	953	1	CWH43_YEAST	P25618 saccharomyc
1480	77.5	5.6	1069	2	Q4IVA6_AZOVI	Q4iva6 azotobacter
1481	77.5	5.6	1118	2	Q9HUE7_PSEAE	Q9hue7 pseudomonas
1482	77.5	5.6	1402	1	K0232_HUMAN	Q92628 homo sapien
1483	77.5	5.6	1551	2	Q447L6_SOLUS	Q447l6 solibacter
1484	77.5	5.6	1646	2	Q5B0U5_EMENI	Q5b0u5 aspergillus
1485	77	5.5	175	2	Q3A0L5_PELCD	Q3a0l5 pelobacter
1486	77	5.5	181	2	Q8ZU94_PYRAE	Q8zu94 pyrobaculum
1487	77	5.5	228	1	CRCB_METCA	Q606p3 methylococc
1488	77	5.5	262	2	Q8KJ17_RHILO	Q8kji7 rhizobium l
1489	77	5.5	268	2	Q35LN3_9BRAD	Q35ln3 bradyrhizob
1490	77	5.5	269	2	Q4B8L9_BURVI	Q4b8l9 burkholderi
1491	77	5.5	269	2	Q393M5_BURS3	Q393m5 burkholderi

RESULT 1

Q6UX65\_HUMAN

ID Q6UX65\_HUMAN PRELIMINARY; PRT; 266 AA.

AC Q6UX65; Q86VD3;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE WWFQ154 (Hypothetical protein TMEM77) (Novel protein).

GN Name=TMEM77; Synonyms=RP5-1180E21.1; ORFNames=RP5-1180E21.1-001,

GN UNQ154;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

RA Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a

bioinformatics assessment.";

RT Genome Res. 13:2265-2270(2003).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Brain, and Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F.; Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Rodriguez S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Eye;

RG NIH MGC Project;

ALIGNMENTS

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Thomas D.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RG NIH MGC Project;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC -----  
DR EMBL; AY358492; AAQ8856.1; -; mRNA.  
DR EMBL; BC047025; AAH47025.3; -; mRNA.  
DR EMBL; AL355816; CAIL9366.1; -; Genomic\_DNA.  
DR EMBL; BC091509; AAH91509.1; -; mRNA.  
DR Ensembl; ENSG0000156171; Homo sapiens.  
KW Hypothetical protein.  
SQ SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;  
  
Query Match 100.0%; Score 1392; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 6e-108;  
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
DB 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
  
QY 61 NIAAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
DB 61 NIAAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
  
QY 121 HVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSV 180  
DB 121 HVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSV 180  
  
QY 181 HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
DB 181 HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
  
QY 241 LHGLTLYDTAPCPINNERTRLLSRDI 266  
DB 241 LHGLTLYDTAPCPINNERTRLLSRDI 266  
  
RESULT 2  
Q4VWF6 HUMAN PRELIMINARY; PRT; 266 AA.  
ID Q4VWF6\_HUMAN  
AC Q4VWF6;  
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Putative transmembrane protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Xu J., Xie Y., Mao Y.;  
RT "Identification of a novel human putative transmembrane protein that is up-regulated in hepatoma."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; AY336747; AAR02410.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
KW Transmembrane.

SQ SEQUENCE 266 AA; 29808 MW; 24E1D5C212C01DF1 CRC64;  
  
Query Match 99.4%; Score 1383; DB 2; Length 266;  
Best Local Similarity 99.6%; Pred. No. 3.4e-107;  
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
DB 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
  
QY 61 NIAAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
DB 61 NIAAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
  
QY 121 HVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSV 180  
DB 121 HVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSV 180  
  
QY 181 HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
DB 181 HSGNFGTDLQKHLWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEAN 240  
  
QY 241 LHGLTLYDTAPCPINNERTRLLSRDI 266  
DB 241 LHGLTLYDTAPCPINNERTRLLSRDI 266  
  
RESULT 3  
Q3ZC48 BOVIN PRELIMINARY; PRT; 266 AA.  
ID Q3ZC48\_BOVIN  
AC Q3ZC48;  
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.  
DT 27-SEP-2005, sequence version 1.  
DT 07-MAR-2006, entry version 5.  
DE Hypothetical protein.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Hereford; TISSUE=Rumen;  
RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,  
RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,  
RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,  
RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,  
RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,  
RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;  
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
CC -----  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC102918; AAI02919.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 266 AA; 29923 MW; A3A00ECE27834855 CRC64;  
  
Query Match 93.0%; Score 1295; DB 2; Length 266;  
Best Local Similarity 90.2%; Pred. No. 7.6e-100;  
Matches 240; Conservative 15; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
DB 1 MWVFOQGLSFLPSALVIWTSAAAFISYITAITLHHVDPVLPYISDTGTVAPEKCLFGAML 60  
  
QY 61 NIAAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAA 120  
DB 61 NIAAVLCVATIIYVRKQVHALNPEENRIIRLNKAGLVGLLSCLGLSILVANFQKTTFFAV 120  
  
QY 121 HVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSV 180  
DB 121 HVCGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVWCGVSASFMLTCSLL 180







QY 1 MWVFOQGLSFLPSALVWITSAAPIFSYITAVTLHHIDPALPYISDTGTGVAPEKCLFGAML 60  
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QY 61 NIAAVLCIATIIYVRKYQVHALSPENVIKLNKAGLVGLILSCGLSIVANFQKTTLFAA 120  
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QY 121 HVSGAVLTFMGSLYMFVQTIYSYQMPKIHGKQVFWIRLLLVICWGSALSMLTCSVVL 180  
|||||  
Db 121 HVCGLVLAFAFMGSFYMFVQTIYSYQMPKIHGKQVFWIRLLLVICWGSALSMMTCSSIL 180  
  
QY 181 HSGNFGTDLQKLNHPEDKGVYLVHMITTAAEWSMSFSFFGFLTYYIRDFQKISLRVEAN 240  
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Db 181 YSSDFGADIVQKLNHPEDKGVYLVHIVTTAAEWSMSFSFFGFLTYYIRDFQKITLRVEAN 240  
  
QY 241 LHGLTYDTAPCPINNERTRLISRD 265  
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Db 241 LHGLTYDTVPCVPTNERTPLLSRD 265

RESULT 6

Q9D520 MOUSE PRELIMINARY; PRT; 267 AA.  
ID Q9D520\_MOUSE  
AC Q9D520;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-2001, sequence version 1.  
DT 07-FEB-2006, entry version 19.  
DE Adult male testis cDNA, RIKEN full-length enriched library,  
DE clone:4930524M19 product:RIKEN cDNA 2610318G18.  
GN Name=2610318G18Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
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RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
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RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner M.,  
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
RA Hill D., Humarick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

RA Sperling S., Stupka E., Sugiyura K., Sultana R., Takenaka Y., Taki K.,  
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563 (2005).  
RL [3]  
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RP STRAIN=C57BL/6J; TISSUE=Testis;  
RC PubMed=16141073; DOI=10.1126/science.1112009;  
RX RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566 (2005).  
RL [4]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Testis;  
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
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RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
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RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).  
RL [5]  
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RP STRAIN=C57BL/6J; TISSUE=Testis;  
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
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RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,









DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE FLJ11259 protein.  
GN Name=FLJ11259;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
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RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton A., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Greenwood J., Schmutz J., Myers R.M.,  
RA Rodriguez A.C., Grimwood J., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Director MGC Project;  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR EMBL; BC018435; AAH18435.1; -; mRNA.  
DR Ensembl; ENSG00000136048; Homo sapiens.  
SQ SEQUENCE 238 AA; 26253 MW; 511875677737F6C0 CRC64;  
  
Query Match 35.4%; Score 492.5; DB 2; Length 238;  
Best Local Similarity 38.8%; Pred. No. 7e-33;  
Matches 97; Conservative 53; Mismatches 79; Indels 21; Gaps 3;  
  
Qy 1 MWVFOQGLSFLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60  
Db 1 MLCFLRGMAFVPLFLVWSSAAFIISYVAVLSGHVNPFLPYISDTGTTPPESGIFGEMI 60  
  
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Db 61 NFSAFLGAATMYTRYKIVQKQNTCYFSTPVENLV-----SLVLGLVGFGMGIVANFQ 114  
  
Qy 114 KTTLFAAHVSGAVLTFGMSLYMFVQTLISYQMOKIHGQVFWIRLLLVICWGSALS 173  
Db 115 ELAVPVVHGGALLAFVCGVVYVTLQSIISYKSCPDWNSLSTCHIRMWISAVSCAAVIPM 174  
  
Qy 174 LTCSSVLHSGNFGTDLEQKLHNWPNEDKGYLVHMTTAAEWSMSFSFFGFLTYYIRDFOKI 233  
Db 175 IVCASLISI-----TKLEWNPREDKYVYHVVSACEWTVAFGFIFFLTFTIQDFQSV 226  
  
Qy 234 SLRVEANLHG 243  
Db 227 TLRISTEING 236

RESULT 11

Q9DC58\_MOUSE  
ID Q9DC58\_MOUSE PRELIMINARY; PRT; 238 AA.  
AC Q9DC58;  
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 2.  
DT 07-FEB-2006, entry version 20.  
DE Adult male lung cDNA, RIKEN full-length enriched library,  
DE clone:1200002N14 product:hypothetical RNA-binding region RNP-1 (RNA  
DE recognition motif) containing protein, full insert sequence.  
GN Name=1200002N14Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Murioidea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
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RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
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RX PubMed=16141072; DOI=10.1126/science.1112014;  
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RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
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RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
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RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
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RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
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RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
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RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
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RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group, and Genome Science Group  
RG (Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense Transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).



[4]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
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Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
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Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[5]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
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RC STRAIN=C57BL/6J; TISSUE=Lung;
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RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK004552; BAB23366.2; -; mRNA.
DR Ensembl; ENSMUSG0000020057; Mus musculus.
DR MGI; MGI:1918962; 120002N14Rik.
DR GO; GO:0003676; F:nucleic acid binding; RCA.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26201 MW; AC89F1301B0A0048 CRC64;
Query Match 34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 8.5e-32;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;
QY 1 MWWFQGLSFLPSALVIVTWSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLCFLRGMAFVPFLVVTWSSAAFIISYVAVLSGHVNPFLPYISDTGTPPESGIFGFI 60
QY 61 NIAAVLCIATIVRYKQV-----HALSPEENVIIKLNKAGLVGLSLCLGLSIVANFQ 113
Db 61 NFSAFLGAATMYTRYKIVEKQNETCYFSTPVPVNLV-----SLALGLVGCIGMGIVANFQ 114
QY 114 KTTLFAAHVSGAVLTFGMGSLYMFVQTTLSYQMPKIHGKQVFWIRLLLVICGVSALS 173
Db 115 ELAVPVVDGGALLAFVCGVVYTLLOSISYKSCPQWNLSLTTCHVRMAISAVSCAAVPM 174
QY 174 LTCSSVLHSGNFGTDLQKLNHPEDKGYVLHMITTAAEWSMSFSFFGFLTYYIRDFOKI 233
Db 175 IACASLISI-----TKLEWNPKEKDYIYHVVSACEWTVAFGFIFYFLTFIQDFQSV 226
QY 234 SLRVEANLH 242
Db 227 TLRISTEIN 235
RESULT 12
Q5XJL0 BRARE
ID Q5XJL0\_BRARE PRELIMINARY; PRT; 240 AA.
AC Q5XJL0;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Zgc:101811.
GN ORFNames=zgc:101811;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI\_TaxID=7955;
RN [1]





